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(54) Targeted delivery through a cationic amino acid transporter

(57) The invention relates to the targeted delivery of substances to cells. The invention provides a virus-like particle or gene delivery vehicle provided with a ligand capable of binding to a human amino acid transporter. Provided are for example ligands that can bind to the human transporter of cationic L-amino acids (hCAT1). Such hCAT1 binding molecules find applications in the design of vector systems for entry into human or primate cells. Preferred are retroviral envelope molecules, which - when incorporated in a virus particle - can infect hCAT1 positive cells at high frequencies. Also within the scope of the invention are methods for the design of such hCAT1 binding molecules.

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Description

[0001] The invention relates to the targeted delivery of substances to cells.

[0002] Delivery of substances to cells allows specific treatment of said cells with compounds that act in the targeted cell. For example, tumour cells, when targeted with toxic components, selectively die when said toxin is delivered to said cell. Yet other cells, when provided with a gene lacking in said cell, can be restored in their function, so-called gene therapy.

[0003] Delivery of a compound to a cells preferably occurs with a vehicle or particle that effectively brings the compound to the desired cell or cells and than delivers said compound into that cell (in vivo or in vitro) where it can exert its action. For this purpose, for example particles such as virus-like particles are suited. These particles, often derived from known viruses, such as retrovirus or adenovirus, are small enough to penetrate in-between tissues and cells and arrive at a cell of choice where it for example can fuse with said cell and deliver its compound. Said virus-like particles may or may not be infectious in themselves, their main concern is the targeted delivery of the compound of interest, such as a gene, a toxin or immunostimulating components such as antigens.

[0004] Yet other examples are gene-delivery vehicles, specifically designed to transfer a gene to a cell of interest. Virus-like particles capable of delivering a gene are examples of said gene-delivery vehicles, however, also other examples of such vehicles, of non-viral origin, such as liposomes or microbodies, or even latex particles, are known. Vehicles such as liposomes or microbodies can of course also carry other compounds than a gene, in particular toxic or immunostimulating components such as antigens can be included in such a vehicle.

[0005] These vehicles or particles all have in common that they need to be provided with a molecule or fragment thereof (ligand) capable of binding with said targeted cell, allowing targeting of said particle or vehicles to cells. There is a need for specific or broadly applicable ligands that react with cell-surface receptors on cells. In particular there is a need for ligands that react with cell-surface receptors after which efficient transfer of said compound to said cell, such as a gene, is possible. Especially in human medicine, such a ligand would enable better application of gene-transfer therapy than is possible now.

[0006] It has been a long-standing objective to exploit retrovirus technology in human gene therapy applications. However, the infection spectrum of retroviruses limits the applications of these viruses in such applications. All known env variants have a rather broad infection spectrum in common. Here lies one of the major shortcomings of current recombinant retrovirus technology. For the purpose of gene therapy, retroviruses are very useful vehicles for the transfer of therapeutic sequences, if proper ligand-receptor targets were available. In conclusion, the concept of the use of retroviruses in human gene therapy is well documented (Gordon and Anderson, 1994; Havenga et al., 1997; Vile et al., 1996). However, it would be clearly advantageous and desirable to devise a strategy for targeted delivery of retroviruses, and modification of the infection spectrum.

[0007] The invention provides a virus-like particle or gene delivery vehicle provided with a ligand capable of binding to a human amino acid transporter. The invention provides said particle or vehicles wherein said ligand comprises peptide molecules or fragments thereof binding said transporter, for example to hCAT1. The peptides or fragments thereof can bind to for example the third extracellular domain of the cationic amino acid transporter hCAT1 or can bind to cells expressing this domain of hCAT1 protein on their extracellular cell surface. These hCAT1 binding molecules can be peptides or antibody fragments displayed on a filamentous phage or as free molecules. In a preferred embodiment, the invention provides a virus-like particle or gene delivery vehicle for delivery of genes to human cells, however, it is also possible to provide said particles or vehicles with other compounds, such as toxins for selective killing or antigens for immunisation.

[0008] In a particular embodiment of the invention, a virus-like particle or gene delivery vehicle is provided comprising at least one viral protein provided with said ligand. Included in the present invention is the use of hCAT1 binding ligands to provide a particle or vehicle that employs hCAT1 to enter a hemopoietic stem cell or any other cell expressing hCAT1. hCAT1 ligands can be incorporated in the envelope of a retrovirus or the capsid of any other viral or non-viral gene transfer vehicle such as an adenoviral vector. Incorporation of these hCAT1 binding sequences can be done using techniques known in the art.

[0009] The invention provides a virus-like particle or gene delivery vehicle wherein said viral protein comprises an envelope protein. In a preferred embodiment the invention provides a a mutant retroviral envelope that is derived from a wild-type ecotropic envelope and which employs hCAT1 to enter the human or primate cell by binding to hCAT1. Such a new retroviral envelope molecule, when incorporated in a retroviral virion, will be able to infect hCAT1 positive cells such as human PHSCS at high efficiencies. The mutant retroviral envelopes can be used to pseudotype recombinant type C retrovirus including but not limited to murine leukemia retroviral vectors. In a further embodiment of the present invention these hCAT1 binding envelopes can also be used to pseudotype lentiviral vectors including equine or HIV derived lentiviral vectors (Kim et al., 1998; Rizvi and Panganiban, 1992), (Kafri et al., 1997; Poeschla et al., 1996), (Miyoshi et al., 1997; Naldini et al., 1996b). Any hCAT1 ligannds or binding envelope molecules or parts thereof made according to the methods described herein or other methods can be ligated into full length mammalian retroviral enve-

lope expression constructs and introduced in cell lines expressing and containing all the sequences necessary for the generation of infectious and functional retroviral particles, in a preferred embodiment the invention provides a virus-like particle or gene delivery vehicle derived from a retrovirus.

[0010] In yet another embodiment, the invention provides a virus-like particle or gene delivery vehicle wherein said viral protein comprises a capsid protein. hCAT1 binding sequences or ligand can also be incorporated in the capsid proteins of adenovirus including but not limited to the HI loop of the knob domain of an adenovirus (Krasnykh et al., 1998) preferably an adenovirus which does not bind to the adenoviral receptor CAR1 or MHC1. This results in an adenovirus that enters cells through hCAT1. Deduced from mCAT1 absent expression in mouse liver (Closs et al., 1993) an hCAT1 binding adenovirus does not exhibit liver transduction when administered *in vivo*. By combining an hCAT1 targeted knob with a ligand for another *in vivo* target hCAT1, targeting of an adenovirus can remove an important limitation of in vivo use of adenoviral vectors for gene therapy (Sullivan et al., 1997). In another embodiment an hCAT1 targeted adenovirus will more efficiently transduce cells that are difficult to transduce such as endothelial cells or smooth muscle cells as compared to a wildtype adenoviral vector including but not limited to an adenoviral vector derived from the adenoviral serotype 5, the invention provides a virus-like particle or gene delivery vehicle derived from an adenovirus.

[0011] An hCAT1 targeted adenovirus is useful for local applications of adenoviral vector such as in patients with restenosis following balloon angioplasty where smooth muscle cells need to be transduced with for example an adenoviral vector carrying the ceNOS cDNA. More efficient transduction of these tissues results in lower multiplicity's of infections (MOIs) that can be used and therefore less vector associated toxicity to the tissues surrounding the target cells (PCT/EP98/00723).

[0012] In a preferred embodiment, the invention provides a virus-like particle or gene delivery vehicle according to the invention wherein said amino acid transporter is a cationic amino acid transporter, preferably a human cationic amino acid transporter-1 (hCAT1) . In a preferred example of the invention provided in the experimental part, the invention provides a virus-like particle or gene delivery vehicle wherein said ligand comprises an amino acid sequence selected from Table 2, preferably from the last four different sequences of Table 2 or a sequence functionally related thereto. Various examples of a ligand having hCAT1 binding activity are provided, a particularly strong example is a ligand comprising at least a part of, comprising minimally 5, more preferably minimally 7 amino acids of the amino acid sequence SVSVGMKPSPRP.

[0013] In yet another embodiment, the invention provides a virus-like particle or gene delivery vehicle according to the invention wherein wherein said ligand comprises a fragment derived from a phage displaying at least one antibody fragment selected for its capacity to bind with said amino acid transporter, in particular a virus-like particle or gene delivery vehicle is provided wherein said antibody fragment comprises an amino acid sequence as shown in Figure 16 or a an amino acid sequence functionally equivalent thereto or obtainable by a method as described in the experimental part of this description.

[0014] The invention also provides use of a virus-like particle or gene delivery vehicle according to the invention in gene-transfer therapy. In numerous gene therapy applications targeted delivery of genes into defined cells is provided by the invention, most notably in the case of in vitro gene transfer into cell types present with low abundance in cell mixtures and in approaches for in vivo gene transfer into cells in a living animal body. In a particular embodiment, the particles or vehicles provided by the invention are used for gene therapy using hCAT1 mediated gene transfer including but not limited to mammalian smooth muscle cells or hemopoietic stem cells such as CD34+CD38- or CD34+(CD33CD38CD71)- cells, including but not limited to adenoviral or retroviral gene transfer vehicles.

[0015] The invention also provides a method for selecting a filamentous phage expressing a protein capable of binding to a ligand comprising constructing a phage library, enriching said library for phages having desired binding characteristics by at least one round of selection of phages for their capacity to bind to a synthetic peptide derived from said ligand, further comprising enriching said library for phages having desired binding characteristics by at least one round of selection of phages for their capacity to bind to a cell expressing said ligand.

[0016] The invention for example provides a peptide phage display to select hCAT1 binding peptides for incorporation in a ligand. To isolate peptides that bind to the third extracellular domain of we employed peptide phage display. A 12 mer peptide phage display library was purchased from New England Biolabs. This library is constructed in the filamentous E. coli phage m13 and the peptide sequences are displayed as N-terminal fusion proteins with the minor coat protein pIII. The unamplified library had a complexity of 1.9×10^9 different sequences as determined by the suppliers. We amplified the library once before using it to select hCAT1 binding peptide phages. Two targets were used to select for peptide displaying phages which bind to the third extracellular domain of hCAT1. First the predicted third extracellular domain of hCAT1 was synthesised as a synthetic peptide by Neosystem, Strassbourg, France. The N-terminus of this peptide was biotinylated and followed by three amino acid linker residues KRR, followed by the predicted sequence of the third extracellular domain. Secondly we generated cell lines derived from the human 911 cell line that overexpress hCAT1 as judged by steady state mRNA expression levels. The hCAT1 expression construct hATRCC1 which is a pcDNA3 based expression construct of the hCAT1 cDNA was employed to transfect 911 cell lines followed by selection for neomycine resistance. A cloned cell line designated k08 was isolated which expresses high levels of hATRCC1

derived hCAT1 mRNA.

[0017] The invention is further described in the experimental part of this description which is not limiting the invention thereto.

Experimental part

[0018] Retroviruses are RNA viruses which efficiently integrate their genetic information into the genomic DNA of infected cells via a reverse-transcribed DNA intermediate. This property of their life-cycle and the fact that parts of their genetic material can be replaced by foreign DNA sequences make retroviruses one of the most promising vectors for the delivery of genes in human gene therapy procedures, most notably for gene therapies which rely on gene transfer into dividing tissues. Most retroviral vector systems are based on mouse retroviruses and consist of two components, i.e. (i) the recombinant retroviral vector carrying the foreign sequences of interest, and (ii) so-called packaging cells expressing the structural viral proteins of which the encoding sequences are lacking in the retroviral vector. Expression of (i) in (ii) results in the production of recombinant retroviral particles capable of transducing susceptible target cells.

[0019] The infectivity and host cell range of the retrovirus particle is conferred by an envelope glycoprotein which specifically binds to a receptor molecule on the target cell membrane. The envelope glycoprotein of all known retroviruses consists of two associated peptides, which are derived by proteolytic cleavage from the same precursor protein encoded by the retroviral envelope (env) gene (Gunzburg and Salmons, 1996; Weiss, 1996) . The amino terminal domain encompasses specific binding site(s) for its receptor on the target cell membrane, determining the virus host range. Within this domain of about 200 amino acids highly conserved sequences are present that are interrupted by two segments designated VRA and VRB which vary in sequence and length among various mammalian type C retroviruses (Battini et al., 1992). The carboxy terminal peptide, which contains trans-membrane anchor sequences, is assumed to account for the selective uptake of the envelope glycoprotein in the virus particle and to mediate fusion between the virus membrane and - depending on the type of virus - the plasma membrane or intracellular vesicle membrane of the target cell (Januszeski et al., 1997; Thomas et al., 1997). In figure 1 a schematic representation of the structure of MuLV env protein is given. Several envelope glycoprotein variants with different infection spectra for mammalian cells have been identified (Battini et al., 1992).

[0020] There are examples or recombinant viruses carrying an amphotropic or GaLV envelope. Recombinant viruses carrying an amphotropic or GaLV envelope are capable of infecting human and murine cells and are commonly used in gene transfer trials including human gene therapy involving the pluripotent hemopoietic stem cell (PHSC) (Havenga et al., 1997). Gene transfer frequencies into PHSCs of human patients and non human primate animal models have been shown to be extremely low and limit therapeutic stem cell gene therapy (Havenga et al., 1997; Hoogerbrugge et al., 1996; Van Beusechem et al., 1993; van Beusechem et al., 1992).

[0021] One important limiting factor has been shown to be low expression levels of retroviral receptors such as the one mediating entry of amphotropic MuLV retrovirus (GLVR2) (Orlic et al., 1996; van Es et al., 1996). The quiescent state of PHSCs when isolated for ex vivo gene transfer procedures poses another blockade (Knaan-Shanzer et al., 1996). Murine stem cell gene therapy experiments have traditionally been performed with ecotropic MuLV vectors (Havenga et al., 1997). Recombinant viruses carrying an ecotropic envelope are only capable of infecting murine cells. Transfer of genes into murine PHSCs using ecotropic retroviral vectors has been shown to result in high transduction efficiencies in circulating PHSC derived peripheral blood cells (PBL). The transduction efficiencies are high enough to be therapeutic if achieved in human PHSCs reaching levels of PHSC gene transfer varying between 30-80 %.

[0022] A small number of studies have been performed in which the transduction efficiency into murine PHSCs of ecotropic and amphotropic retroviruses were actually compared directly (Havenga et al., 1997). One of these studies indicated that infection with amphotropic retrovirus resulted in expression and thus transgene presence for less than 8 weeks whereas infection with ecotropic virus resulted in expression for more than 44 weeks after transplantation (Demarquoy, 1993). In a similar study, ecotropic virus was shown to be approximately 50 fold more efficient in transducing murine PHSCs as compared to amphotropic retrovirus (Orlic et al., 1996).

[0023] Ecotropic and amphotropic retrovirus differ in the receptor that is employed for virus entry (Albritton et al., 1989; van Zeijl et al., 1994). Ecotropic virus binds target cells via the ecotropic receptor mCAT1 which is a transporter of cationic L-amino acids (Kim et al., 1991) and amphotropic retrovirus binds target cells via the amphotropic receptor GLVR2, a sodium dependent phosphate transporter GLVR2 (Kavanaugh et al., 1994; Miller and Miller, 1994; van Zeijl et al., 1994).

[0024] A comparative study measuring mRNA levels of both the ecotropic and amphotropic receptors in mouse PHSCs (lit c-kitbright) revealed an important difference. This study demonstrated that ecotropic receptor (mCAT1) mRNA levels in these cells are high whereas amphotropic receptor (GLVR2) mRNA levels were undetectable by RT-PCR (Orlic et al., 1996). GLVR2 expression studies on $CD34^+(CD38,CD33,CD71)^-(CD34^+lin$ cells) isolated from human bone marrow, umbilical cord blood and immobilised peripheral blood supports these data (van Es et al., 1996).

[0025] Another important factor which plays a role in determining successful retroviral entry and integration is the

postbinding route of entry of a retrovirus particle. The postbinding entry route for ecotropic virus is different from that of amphotropic retrovirus. Ecotropic retrovirus tranductions are sensitive to lysosomotropic agents such as chloroquine and NH4Cl. This suggests that upon binding of the ecotropic retrovirus, the retrovirus is internalised by receptor mediated endocytosis (McClure et al., 1990). In contrast upon binding of the envelope of amphotropic retrovirus the viral envelope directly fuses with the plasma membrane. This is a process that is not disrupted by lysosomotropic agents suggesting that the postbinding steps of amphotropic MuLV virus are essentially different from those of ecotropic MuLV retrovirus (McClure et al., 1990).

[0026] The human homologue of the murine ecotropic virus receptor mCAT1 is hCAT1. Like mCAT1 mRNA expression in mouse PHSCs, hCAT1 mRNA is expressed at high levels in human PHSCs (Orlic et al., 1996). For both mCAT1 and hCAT1 the normal function is the import of cationic amino acids such as lysine and arginine (Albritton et al., 1993; Malhotra et al., 1996). The third predicted extracellular domain of mCAT1 includes a sequence YGE. The residues are crucial for receptor function. In the nonfunctional hCAT1 the sequence of the third extracellular domain is PGV. Mutation of the human sequence into one or two of the residues of mCAT1 results in a hCAT1 protein with ecotropic receptor function (Albritton et al., 1993; Yoshimoto et al., 1993). See also figure 2.

[0027] A number of mutant ecotropic envelope molecules have been described in the literature. MacKrell et al have mutated amino acids within the receptor-binding domain VRA of ecotropic MuLV envelope in order to identify residues involved in receptor binding. Virions incorporating mutant envelopes carrying mutations at amino acid residue D84 have lost their binding capabilities to the ecotropic receptor mCAT1 (MacKrell et al., 1996). Virions carrying D84 mutated envelope protein were tested on human cells to search for a possible change in receptor recognition specificity but were found not to infect human cells (Mike Januszeski, personal communication).

Skov and Andersen have studied ecotropic Moloney envelope interactions with mCAT1 by generation of mutant envelope molecules with mutated arginine and lysine residues in gp70 including VRA followed by introduction in a replication competent retroviral backbone (Skov and Andersen, 1993).Mutations R135G, K137Q, R157G and R159A (R102G,K104Q,R124G and R126A without signal peptide respectively) resulted in virions that were not able to replicate.

Kingsman et al have described in PCT application WO96/31602 an insertion site in the VRA domain of ecotropic envelope which allows modification of the tropism. An integrin binding sequence was inserted resulting in infection of human cells expressing the respective integrin.

[0028] PVC-211 murine leukemia virus (MuLV) is a neuropathogenic variant of ecotropic Friend MuLV (F-MuLV) that causes a rapidly progressive neurodegenerative disease in susceptible rodents. PVC-211 MuLV, but not the parental F-MuLV, can infect rat brain capillary endothelial cells (BCEC) efficiently, and the major determinant for BCEC tropism of PVC-211 MuLV is localized within the env gene. More specific analysis indicated that E116G and E129K substitutions in the background of the F-MuLV envelope protein were sufficient for conferring BCEC tropism on the virus (Masuda et al., 1996a). Host range changes of these mutations were found to include CHO cells normally not infectable with ecotropic F-MuLV or M-MuLV. The latter suggests that these mutations overcome a negative effect of CAT1 CHO cell receptor glycosylation in the region of virus binding in the third extracellular domain of mCAT1 (Masuda et al., 1996b).

[0029] By employing particular natural env variants the transduction spectrum can be limited to some extend, but true specificity for human target cells of interest can not be obtained following this strategy (Masuda et al., 1996a; von Kalle et al., 1994; Wilson et al., 1994).

[0030] In the present invention we describe the expansion of the host range of an ecotropic retrovirus or other gene transfer vehicle such as an adenoviral vector resulting in increased transduction of hemopoietic stem cells. In this invention, targeted delivery is accomplished by directing the retrovirus particle to cell membrane molecules differing from the natural receptor. This could then lead to increased specificity of transduction.

[0031] The present invention discloses examples of molecules that bind to hCAT1 and that can be used to develop gene transfer vehicles such as retroviral and adenoviral vectors. In particular, the invention relates to proteins and derivatives thereof expressed in the lipid bilayer of enveloped virus particles such as retroviruses. Methods, materials, procedures and pharmaceutical formulations for the design and preparation of the above molecules and virus particles are also part of the invention. These molecules and virus particles have applications in the field of virology, gene therapy, biochemistry and molecular biology.

[0032] The present invention relates to peptide molecules binding to hCAT1. These molecules are characterized by their ability to bind the third extracellular domain of the cationic amino acid transporter hCAT1 either a synthetic peptide encompassing this third extracellular domain or by binding to cells expressing this domain of hCAT1 protein on their extracellular cell surface. These hCAT1 binding molecules can be peptides or antibody fragments displayed on a filamentous phage or as free molecules.

[0033] Included in the present invention are filamentous phages displaying hCAT1 binding molecules and that can be used to transfer gen s into cells by modification of the phage genome using techniques known in the art.

[0034] Included in the present invention is the use of hCAT1 binding molecules to design vectors that employ hCAT1 to enter a HSC or any other cell expressing hCAT1. hCAT1 binding molecules can be incorporated in the envelope of a

retrovirus or the capsid of any other viral or non-viral gene transfer vehicle such as an adenoviral vector. Incorporation of these hCAT1 binding sequences can be done using techniques known in the art.

[0035] Preferred are mutant retroviral envelopes that are derived from wild-type ecotropic envelope and which employ hCAT1 to enter the human or primate cell by binding to hCAT1. These new retroviral envelope molecules, when incorporated in a retroviral virion, will be able to infect hCAT1 positive cells such as human PHSCs at high efficiencies. The mutant retroviral envelopes can be used to pseudotype recombinant type C retrovirus including but not limited to murine leukemia retroviral vectors. In a further embodiment of the present invention these hCAT1 binding envelopes can also be used to pseudotype lentiviral vectors including equine or HIV derived lentiviral vectors (Kim et al., 1998; Rizvi and Panganiban, 1992), (Kafri et al., 1997; Poeschla et al., 1996), (Miyoshi et al., 1997; Naldini et al., 1996b).

[0036] Any hCAT1 binding envelope molecules or parts thereof made according to the methods described herein or other methods can be ligated into full length mammalian retroviral envelope expression constructs and introduced in cell lines expressing and containing all the sequences necessary for the generation of infectious and functional retroviral particles including but not limited to cell lines preferably derived from the adenoviral E1 transformed, human cell line PER.C6 (WO97/00326) and that express murine leukemia gag-pol constructs and a retroviral vector containing long terminal repeats (LTRs), and retroviral RNA packaging signals such as those vectors described in WO96/35798. The hCAT1 binding envelopes made according to the subject material of this invention can also be used to pseudotype vectors other than murine leukemia retroviral vectors including but not limited to lentiviral vectors (Naldini et al., 1996a; Naldini et al., 1996b).

[0037] In a further embodiment of the present invention, hCAT1 binding sequences can also be incorporated in the capsid proteins of adenovirus including but not limited to the HI loop of the knob domain of an adenovirus (Krasnykh et al., 1998) preferably an adenovirus which does not bind to the adenoviral receptor CAR1 or MHC1. This results in an adenovirus that enters cells through hCAT1. Deduced from mCAT1 absent expression in mouse liver (Closs et al., 1993) an hCAT1 binding adenovirus does not exhibit liver transduction when administered *in vivo*. By combining an hCAT1 targeted knob with a ligand for another *in vivo* target hCAT1 targeting of an adenovirus can remove an important limitation of in vivo use of adenoviral vectors for gene therapy (Sullivan et at., 1997). In another embodiment an hCAT1 targeted adenovirus will more efficiently transduce cells that are difficult to transduce such as endothelial cells or smooth muscle cells as compared to a wildtype adenoviral vector including but not limited to an adenoviral vector derived from the adenoviral serotype 5.

[0038] An hCAT1 targeted adenovirus is useful for local applications of adenoviral vector such as in patients with restenosis following balloon angioplasty where smooth muscle cells need to be transduced with for example an adenoviral vector carrying the ceNOS cDNA. More efficient transduction of these tissues results in lower multiplicity's of infections (MOIs) that can be used and therefore less vector associated toxicity to the tissues surrounding the target cells (PCT/EP98/00723).

[0039] In another aspect of the present invention, the hCAT1 binding human FAbs that are part of the subject matter of this invention can be used to measure expression of hCAT1 molecules on cells that are targets for gene therapy using hCAT1 mediated gene transfer including but not limited to mammalian hemopoetic stem cells such as CD34+CD38- or CD34+(CD33CD38CD71)- cells. This could be part of a procedure aimed at determining when or whether a patients cells are most susceptible to gene transfer through hCAT1 including but not limited to adenoviral or retroviral gene transfer vehicles.

[0040] The skilled artisan will be able to apply the teaching of the present invention to other virus capsid or envelope or non-viral gene transfer molecules or vehicles than those exemplified herein without departing from the present invention and therefore the examples presented are illustrations and not limitations. It is intended that all such other examples be included within the scope of the appended claims.

Example 1. Sequences of hCAT1 cDNAs amplified from human CD34+ cells.

[0041] For the purpose of developing gene transfer tools that enter PHSCs through hCAT1, specifically through binding to the third extracellular domain, we isolated total RNA from a number of different human $CD34^+$ samples and determined the cDNA sequence of hCAT1 (see figure 2). Total RNA was isolated according to the protocol described by Chomczynski et al (Chomczynski and Sacchi, 1987). RT-PCR was performed by using the SuperScript Preamplification System for First Strand cDNA Synthesis (Life Technologies). For first strand synthesis random hexamers were used. The hCAT1 cDNA was amplified with two sets of primers, each resulting in a product of approximately 1 kb encompassing the open reading frame of the hCAT1 mRNA (Yoshimoto et al., 1991). DNA sequencing was performed by BaseClear, Leiden, The Netherlands using automated sequence analysis. In figure 3a and 3b the results of sequence analysis of hCAT1 cDNA isolated from $CD34^+$ cells from mobilized peripheral blood or umbilical cord blood are compiled. Clearly from thes⁻ nucleotide sequence analyses (figure 3b) it can be deduced that indeed in the $CD34^+$ samples tested hCAT1 is expressed and includes the third extracellular domain with predicted sequence KNWQLTEEDFGNTSGRLCLNNDTKEGKPGVGGF which includes the sequence PGV determining function as receptor (see above) . There-

fore targeting through this domain or part of this domain of hCAT1 in hemopoietic $CD34^+$ cells including but not limited to hemopoietic stem cells such as defined by lineage negative phenotypes e.g. $CD34^+CD38$ is possible.

Example 2. Peptide phage display to select hCAT1 binding peptides.

[0042] To isolate peptides that bind to the third extracellular domain of hCAT1 (Albritton et al., 1993) (figure 2) we employed peptide phage display. A 12 mer peptide phage display library was purchased from New England Biolabs. This library is constructed in the filamentous E. coli phage m13 and the peptide sequences are displayed as N-terminal fusion proteins with the minor coat protein pIII. The unamplified library had a complexity of 1.9×10^9 different sequences as determined by the suppliers. We amplified the library once before using it to select hCAT1 binding peptide phages. Two targets were used to select for peptide displaying phages which bind to the third extracellular domain of hCAT1. First the predicted third extracellular domain of hCAT1 was synthesised as a synthetic peptide by Neosystem, Strassbourg, France. The N-terminus of this peptide was biotinylated and followed by three amino acid linker residues KRR, followed by the predicted sequence of the third extracellular domain (figure 4). Secondly we generated cell lines derived from the human 911 cell line that overexpress hCAT1 as judged by steady state mRNA expression levels. The hCAT1 expression construct hATRCC1 which is a pcDNA3 based expression construct of the hCAT1 cDNA (Malhotra et al., 1996)was employed to transfect 911 cell lines followed by selection for neomycine resistance in 1 mg/ml of G418 (Genetecin, Life Technologies, Inc). A cloned cell line designated k08 was isolated which expresses high levels of hATRCC1 derived hCAT1 mRNA (figure 5).

[0043] To select for peptide displaying phages that bind to the putative third extracellular domain of hCAT1 as expressed on human cells the following selection procedure was employed. Six rounds of selection on biotinylated hCAT1 peptide (figure 4) followed by three rounds of selection on hCAT1 overexpressing cells k08. Initially two separate selections were carried out differing in the stringency of washing. Low stringency washing consisted of 3 washes with 2 % (w/v) milk powder in PBS with 0.05 % (v/v) Tween 20 and 3 washes with PBS. High stringency washing consisted of 5 washes with 2 % (w/v) milk powder, PBS with 0.05 % Tween 20, 5 washes with PBS, 0.05 % Tween 20 and 5 washes with PBS. After 1 round of selection on 911-hCAT1-k08 cells eluted phages from both washing procedures were pooled and used for a second and third round of selection on 911-hCAT1-k08 cells. The results of these experiments are depicted in table 1. Clearly the ratio of input over output increases upon selection on hCAT1 peptide indicative of selection for binding phages. When selection on hCAT1 positive cells was started the ratio drops and slightly increases in the last round on hCAT1 expressing human cells.

[0044] After the last round of selection with the hCAT1 peptide and after each round of cell selection the pools of peptide displaying phages were tested for binding to immobilized hCAT1 peptide using an Enzyme Linked Immunosorbent Assay (ELISA). 96-well plates were coated with 2 mg/ml biotinylated BSA in PBS and incubated for 1 hour 37 °C after which the wells were rinsed 3x for 5 minutes with PBS/0.05% Tween 20. Then the wells were saturated with streptavidin (10 mg/ml in PBS/0.5% gelatin) for 1 hour at room temperature (RT) and washed 3 times with PBS/0.05 % Tween 20. Then the wells were incubated overnight at 4 °C with biotinylated hCAT1 peptide (figure 4) at a concentration of 10 mg/ml in PBS. The next day the wells were rinsed two times with PBS/0.1 % Tween 20 and 2x with PBS. Then the wells were blocked with 2% non-fat milkpowder in PBS for at least 30 minutes at RT followed by three rinses with with PBS/0.1 % Tween and three with PBS. Subsequently an equal volume of 4% non-fat milkpowder in PBS was added to all wells and culture supernatant or purified phage (PEG precipitated) and incubated for 1.5 hours at RT. After this incubation the wells were washed three times with PBS/0.1 % Tween 20 and three times with PBS followed by incubation with an anti-m13 antibody solution (Pharmacia, 1:5000 in 2% non-fat milkpowder in PBS) for 1 hour at RT. Again the wells were washed three times with PBS/0.1 % Tween and three times with PBS followed by the addition of a rabbit-anti goat HRP conjugate solution (BioRad, 1:2000 in 2% non-fat milkpowder in PBS) for 1 hour at RT. After this incubation the wells were washed again three times with PBS/0.1% Tween and three times with PBS. Detection of phage binding was then visualized using TMB colour solution (0.1 mg/ml TMB, 1% DMSO, 1x TMB buffer, 0.001% 30% H_2O_2 in H_2O) 20-30 min in the dark at RT and stopped with 2 N H_2SO_4 and read at 450 nm in a microplate reader. Using this hCAT1 specific ELISA an enrichment of phages binding to hCAT1 peptide is achieved (figure 6). Importantly after binding of the peptide selected pools to hCAT1 overexpressing cells eluted phages still bind to hCAT1 peptide. Clones isolated from round 3 on hCAT1 overexpressing cells were isolated and tested on hCAT1 peptide ELISA (figure 7). Except 1, all tested clones bound to hCAT1 peptide and thus to the third extracellular domain displayed on human cells.

[0045] To confirm enrichment for specific sequences and to determine the amino acid sequence of the 12 mer peptides displayed, we isolated single stranded m13 phage DNA for automated sequence analysis (Baseclear, Leiden, The Netherlands). The oligonucleotide used for sequencing was 5'-CCCTCATAGTTAGCGTAACG-3'. We sequenced clones isolated from the pools of various peptide and cell selections. For this purpose we pooled the eluates of the two different washing conditions. In addition to the amplified 12 mer peptide library w only selected clones from peptide rounds 3 ,5 and 6 and cell rounds 1,2 and 3. In table 2 the sequences determined for the various clones are given. Clearly a very strong selection occurred because all cell selected phage clones displayed one sequence namely: SVSVGMKPSPRP.

This sequence is also displayed by phages in hCAT1 peptide selected pool 6 in a mixture with 3 other sequences. These other phages are lost once the phage pools selected on hCAT1 peptide are selected for binding to hCAT1 over-expressing cells.

[0046] The cloned SVSVGMKPSPRP displaying m13 phage was used in experiments to measure binding of the displayed sequence to cells that express hCAT1. First we did an experiment using the flow cytometer and the 2 cell lines 911-pcDNA3 and 911-hCAT1(k08) . Cells were incubated with 10^{11} phage in 100 ml PBS/0.1% BSA for 1 hour at room temperature. Subsequently the cells were washed twice with PBS/0.1 % BSA followed by incubation of the cells with anti-m13 antibody (Pharmacia, 1:500 in PBS/0.1 % BSA) for 30 min at room temperature and washed twice with PBS/0.1 % BSA. Then the cells were incubated with rabbit-anti goat FITC (DAKO, 1:50 in PBS/0.1 % BSA) for 30 min at RT and washed twice with PBS/0.1 % BSA. Binding of phage was then measured in the FL1 channel of a Becton and Dickinson flow cytometer. As a control we used an identical amount of phage from the amplified 12 mer libary. In figure 8 the results of this experiment are depicted. Clone #26 phage binds to 911 cells and in particular to 911 cells that over-express hCAT1.

[0047] We also measured cell binding of phage incubating hCAT1 expressing cells with phage followed by titering total cell bound phage, eluted phage and cell associated phage fractions on E.coli using a standard m13 plating assay on a lawn of E.coli cells. For this purpose E.coli strain ER2537 is grown overnight in LB medium. This overnight culture is then used to inoculate 20 ml of fresh LB medium at an OD_{600nm} of 0.05. Once at an OD_{600nm} of 0.5 500 ml of the ER2537 E.coli bacteria were mixed with 500 ml dilutions of phage samples and incubated at RT for 10 min. Plating on a standard LB-agar plate was performed by mixing 3 ml top agar with 200 ml of each sample. Once the topagar was solidified the plates were transferred upside down to a 37 °C incubator for 12-14 hours. Plaques were counted and used to determine the number of phage particles binding to hCAT1 expressing cells. In table 3 cell binding is depicted.

[0048] Clearly from these results we can conclude that the 12 mer peptide displaying phage with sequence SVSVGMKPSPRP indeed binds to hCAT1 expressing cells. hCAT1 expressing Cells were also incubated at 37 °C followed by elution of bound phages plus cell associated phages were liberated. Both were used in phage titering on E.coli and clearly a cell associated fraction is detected. This suggests that the phage displaying sequence SVSVGMKPSPRP and which bind to hCAT1 also enter a human hCAT1 expressing cell. This feature of sequence SVSVGMKPSPRP could be used for the development of gene transfer products useful in gene therapy.

Example 3. Human FAb phage display to select hCAT1 binding human antibody molecules.

[0049] To isolate antibodies that bind to the third extracellular domain of hCAT1 (Albritton et al., 1993) (figure 2,4) we employed phages displaying human FAb fragments encompassing the light and heavy variable and constant regions. A human FAb phage display library was constructed in phage display vector pCES1 a vector derived from pCANTAB6 (McGuiness et al., 1996). The library was constructed in the filamentous E. coli phage m13 and the FAb sequences are displayed partly as N-terminal fusion proteins with the minor coat protein pIII. The unamplified library had a complexity of approximately 3.3×10^{10} different sequences. Two targets were used to select for peptide displaying phages which bind to the third extracellular domain of hCAT1. First the predicted third extracellular domain of hCAT1 was synthesized as a synthetic peptide by Neosystem, Strassbourg, France. The N-terminus of this peptide was biotinylated and followed by three amino acid linker residues KRR, followed by the predicted sequence of the third extracellular domain (figure 2,4). Secondly we generated cell lines derived from the human 911 cell line that overexpress hCAT1 as judged by steady state mRNA expression levels. The hCAT1 expression construct hATRCC1 which is a pcDNA3 based expression construct of the hCAT1 cDNA was employed to transfect 911 cell lines followed by selection for neomycine resistance in 1 mg/ml of G418 (Geneticin, Life Technologies, Inc) . A cloned cell line designated k08 was isolated which expresses high levels of hATRCC1 derived hCAT1 mRNA (figure 5).

[0050] To select for FAb displaying phages that bind to the putative third extracellular domain of hCAT1 as expressed on human cells the following selection procedure was employed. Four rounds of selection on biotinylated hCAT1 peptide (figure 4) followed by three rounds of selection on hCAT1 overexpressing cells k08. For selection on biotinylated hCAT1 peptide 250 ml of FAb library (or eluted phage from the previous round) was mixed with 250 ml 4% Marvel in PBS and equilibrated while rotating at RT for 1 hour. Subsequently biotinylated hCAT1 peptide (20-500 nM in H_2O) was added. This mix was incubated on the rotator at RT for 1 hour before 250 ml equilibrated streptavidin-dynabeads in 2% Marvel in PBS was added. After incubation on a rotator at RT for 15 min the beads with the bound phage were washed 5 times with PBS/2% Marvel/0.1% Tween, 5 times with PBS /0.1% Tween and 5 times with PBS. Then the phage were eluted by incubation with 0.1M Tri-ethyl-amine on a rotator at PT for 10 min and neutralised in 1 M Tris-HCl pH 7.4. The eluted phage were titered and amplified in TG1 before the next selection. For selection on 911-hCAT1 cells, the cells were harvested at a confluency of about 80 % and suspended in PBS/10 % FBS/2 % Marvel to a final concentration of at least $3x10^6$ cells/ml. This cell suspension was incubated for 30 min on a rowing boat mixer (or rotator), while at the same time phage were also preincubated in PBS/10 % FBS/2 % Marvel. Then the cells were centrifuged, resuspended in the preincubated phage solution and incubated on a rowing boat mixer (or rotator) for 1 hour. Afterwards the cells

were washed 10 times with PBS/10 % FBS/2 % Marvel and twice with PBS. The cells were centrifuged and resuspended in 0.6 ml water. Subsequently 0.6 ml 200 mM triethylamine was added (dropwise while vortexing). After 5 minutes the suspension was neutralised by adding 0.6 ml of 1 M Tris-HCl pH 7.4 (dropwise while vortexing).After cenrifugation (5 min, 14000 rpm) the supernatant was transferred to a new tube and titered and amplified in TG1 before the next selection. The results of these experiments are depicted in table 4. clearly the ratio of input over output increases upon selection on hCAT1 peptide indicative of selection for hCAT1 peptide binding phages. When selection on hCAT1 positive cells was started the ratio dropped and slightly increased in the last round on hCAT1 expressing cells.

[0051] The pools of the last 3 rounds were tested for binding to the biotinylated hCAT1 peptide in a hCAT1 specific ELISA and also for cell binding by flow cytometric analysis (both protocols are described in example 2). After the last round of selection on cells the pool of FAb phages still binds to the biotinylated hCAT1 peptide (figure 9). Flow cytometric analysis showed that this pool also binds to hCAT1 overexpressing cells (figure 10). From this pool 43 clones were analysed by fingerprint analysis and divided into 14 different groups. From each group 1 phage clone was tested for binding to the biotinylated hCAT1 peptide in a hCAT1 specific ELISA and also for cell binding by FACS analysis. Three clones appeared to be streptavidin binders whereas the other 11 clones showed binding to the biotinylated hCAT1 peptide (figure 11). Flow cytometric analysis revealed that only 1 of the 14 clones showed strong binding to hCAT1 overexpressing cells (figure 12). This clone was analyzed in more detail (figures 13,14). Clearly clone #25 binds strongly to the synthetic hCAT1 peptide used and to hCAT1 overexpressing 911 k08 cells. Moreover average fold increased binding of this phage to 911-hCAT1-k08 overexpressing cells over 911-pcDNA3 cells was found to be 1.6 ± 1.2 fold (figure 14). Double strand phagemid DNA was prepared and used to determine the nucleotide and deduced amino acid sequence of the displayed variable heavy and light chains. For a schematic picture of the vector pCES1 in which the library of variable chains was cloned (see figure 15). The hCAT1 binding domains are as expected homologous to human immunoglobulin sequences. The complementarity determining regions (CDRs) are indicated in figure 16.
The sequences of this immunoglobulin can be incorporated in viral or non-viral proteins that mediate binding and entry to cells and thus create gene transfer vehicles that enter cells through hCAT1. The hCAT1 binding human FAbs can also be used to measure expression of hCAT1 on cells that are targets for gene therapy using hCAT1 mediated gene transfer.

Example 4 Incorporation of hCAT1 binding peptides in ecotropic retroviral envelope

[0052] To include hCAT1 binding peptides (see example 2) in the context of an ecotropic murine leukemia viral envelope we used functional display of ecotropic envelope by filamentous phages. We used the construct gpIII/env2 which encodes a fusion protein consisting of a prokaryotic signal peptide and all of the gp70 protein including the variable regions A and B and the polyproline hinge (amino acid residues 34-308) fused to the capsid protein encoded by gene III of m13. Numbering of amino acid sequences was done according to the unprocessed envelope sequence as deposited in the Swiss prot database with accession number P03385 and starting from the viral signal peptide. In table 5 all the oligonucleotides are depicted that are used for insertion of the peptide sequences in retroviral envelope.

[0053] Three sites and ways of peptide insertion have been chosen: (1) Insertion at the BstEII site of the ecotropic envelope. (2) Replacement of sequence PFSS (residues 96-99) by each of the 4 the peptides (see table 5). (3) Replacement of sequence LTSLTP (residues 122-127) by each of the 4 peptide sequences peptides (see table 5). The sequences PFSS and LTSLTP are predicted to be on displayed on the outside of the envelope protein as deduced from the structure of crystallised Friend ecotropic envelope (Fass et al., 1997). For the BstEII insertion constructs the two single stranded complementary oligonucleotides were synthesised. At the amino acid sequence level linker amino acids were included at the amino and carboxyterminus of the inserted peptide sequence. These single stranded oligonucleotides were then mixed in equimolar fashion heated to 95 °C and slowly cooled to room temperature to allow hybridisation of the complementary molecules to double stranded DNA. Annealing was followed by BstEII digestion and separation on a 2 % agarose gel run in TAE-buffer. DNA was then excised from the gel and purified using Qiaquick gel extraction kit (Qiagen,Germany). At the same time double stranded phagemid DNA of construct gpIII/env2 was digested and thus linearized with BstEII. Linearized gpIII/env2 DNA was subjected to an incubation with the thermosensitive alkaline phosphatase TSAP (Life technologies), then mixed in various molar ratios with double stranded BstEII digested oligonucleotides encoding any of the 4 hCAT1 binding peptides (see table 5b).Then 1 unit of T4 ligase and T4 ligase buffer supplemented wit 1 mM ATP as added. The ligation mixture was incubated for 1 hour at + 20 °C. The ligation mixtures were then transformed into Max DH5a competent bacteria (Life technologies). Ampicillin resistant colonies were picked and subjected to a PCR with one of the 4 primers in table 5c and primer Ecoenv12 (see table 5). This PCR allows one to determine the nature of the inserted sequence and its orientation. Plasmid DNA of colonies with correct orientation of insert DNA was then isolated using Qiagen columns and sequenced (Baseclear, Leiden) to confirm the complete sequence of the inserts and boundaries plus their orientation.

[0054] For the insertion/deletion of hCAT1 binding peptide sequences into gpIII/env2 at the LTSLTP and PFSS posi-

tions two fragments were amplified (primary PCR) using Elongase polymerase and the following two pairs of primers: Fragment 1: Eco nv17 (sense primer, table 5c) plus one of the even numbered oligonucleotides in table 5a. Fragment 2: Ecoenv12 or ecoenv05 (antisense, table 5c) plus an odd numbered primer in table 5a. Fragment 1 harbours at the DNA lev I the 3' end whereas fragment 2 harbours the peptide insertion at the 5' end. Because both fragments have identical 3' (fragment 1) and 5' ends (fragment 2) they can be used to assemble a full double stranded DNA fragment encompassing the ecotropic envelope sequence between and including part of the ecoenv17 and ecoenv12 oligonucleotide sequences. This is done by first purifying the two fragments from the primary PCR using Qiaquick PCR purification columns to remove all remaining primers followed by doing a PCR using the two overlapping fragments, and primers ecoenv17 and ecoenv12, and all the components necessary for DNA amplification using Elongase. This step results in the assembly of a fragment harbouring the 12 mer hCAT1 binding peptide insertions and result in the deletion of the LTSLTP or PFSS sequence. These fragments are purified and digested with NotI and PinA1 resulting in a DNA fragment of approximately 519 basepairs which was isolated from an agarose gel using Qiagen DNA isolation kit. The 519 basepair fragments were then ligated into a NotI and PinA1 digested gpIII/env2 Surfscript fragment of approximately 4000 basepairs using T4 ligase as described above in example 3. E coli bacteria are then transformed with the ligation mixture, ampicillin colonies picked, plasmid DNA isolated and analyzed for the presence of 519 basepair inserts using Not1 and PinA1 restriction enzymes and DNA agarose gel electrophoresis. Plasmids with appropriate inserts were then further verified by automated DNA sequencing of the inserts (Baseclear, Leiden).

[0055] Phages displaying envelope with the various peptide inserts can then be produced and tested for their binding to and entry of hCAT1 expressing cells and compared to phages displaying the gpIII/env2 construct. The hCAT1 binding envelopes can then be used to develop retroviral vectors produced by mammalian cell lines.

Example 5 Soluble FAb generation and binding to human cells

[0056] To prepare soluble FAb fragments of the hCAT1 binding FAb phage clone periplasmic fractions were made from HB2151 bacteria infected with clone # 25 phage. Infected bacteria were grown in LB medium with 2% glucose and 100 mg/ml ampicillin (LBGA) overnight while shaking at 30 °C. The next day the infected cells were diluted 1:100 in 50 ml fresh LBGA and grown at 37 °C until the OD_{600} was 0.8. Bacteria were then pelleted followed by resuspension in 25 ml LB, 100 mg/ml ampicillin and 1 mM IPTG and incubation for 3 hours at 30 °C while shaking vigorously. Then the bacteria were pelleted and resuspended in 1 ml ice-cold PBS followed by a 14-16 hour incubation at 4 °C while rotating. The next day the periplasmic fraction was cleared from bacterial residues by centrifugation: once for 10 minutes at 8000 rpm C (Eppendorf centrifuge #5402) at 4 °C followed by a spin of 10 minutes at 14000 rpm, 4 °C . Then the FAb periplasmic fractions were aliquoted and stored at -20 °C. The presence and expression of FAb fragments was confirmed by doing a dot blot and probing for human kappa light chains with anti-human kappa polyclonal rabbit antibodies (Dako A0191, 1:1000 dilution, 60 minutes) and anti rabbit IgG (H + L) antibodies conjugated with horse radish peroxidase (Biorad, 170-6515, 1:20.000, 60 minutes). Each step was followed by washing 6 times with PBS, 0.05 % Tween 20 (v/v). Final detection of human FAbs was done using ECL staining (Amersham). This revealed the presence of high concentrations of soluble FAb fragment of hCAT1 binding clone # 25. Dilutions of antibodies were made in PBS, 0.5 % BSA (w/v) , 0.05 % Tween 20 (v/v).

[0057] The FAb fractions made as described above were then used to perform flow cytometric analyses in 911-hCAT1-k08 cells expressing hCAT1 and compared to phages displaying clone 25 (see example 3) (figure 17). For this purpose cells were incubated with 100 ml periplasmic fraction of clone 25 or control clone for 1 hour at room temperature followed by washing twice with PBS, 0.1 % BSA and incubation with 500 times diluted anti-human kappa light chain antibodies (see above) for 30 minutes at room temperature. This was followed by washing twice with PBS/0.1 % BSA and a 30 minute room temperature incubation with goat-anti-rabbit immunoglobulin antibodies conjugated with phycoerythrin (diluted in 1:20 in PBS/0.1 % BSA, Sigma P9795) and measurement in a flow cytometer. Detection of phage binding was done as described under example 2.

[0058] Clearly FAb preparations of clone 25 bind to hCAT1 expressing cells whereas FAb fragments of an irrelevant CHO cell binding clone did not. The results are very similar to the results observed with phages displaying FAb clone 25 (figure 17). Compared to phages displaying hCAT1 binding FAb 25, FAb fragments of clone 25 facilitate the measurement of hCAT1 in a multiparameter setting such as $CD34^+$ or $CD34^+$lin cells.

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Table 1

	Stringent selection			Non-stringent selection		
Selection	**Input phages**	**Output phages**	**Output input**	**Input phages**	**Output phages**	**Output input**
500 nanoM peptide	1.4×10^{10}	0.6×10^{5}	4.3×10^{-6}	1.4×10^{10}	1.5×10^{5}	1.1×10^{-5}
500 nanoM peptide	3.8×10^{9}	1.1×10^{6}	2.9×10^{-4}	3.8×10^{8}	9.8×10^{5}	2.6×10^{-3}
500 nanoM peptide	7.6×10^{7}	3×10^{4}	3.9×10^{-4}	3.8×10^{7}	9.0×10^{3}	2.4×10^{-4}
500 nanoM peptide	2.1×10^{8}	6×10^{5}	2.9×10^{-3}	1.1×10^{8}	6.8×10^{5}	6.2×10^{-3}
100 nanoM peptide	5.3×10^{10}	2.4×10^{9}	4.5×10^{-2}	6.7×10^{10}	1.5×10^{9}	2.2×10^{-2}

Table 1 (continued)

	Stringent selection			Non-stringent selection		
Selection	**Input phages**	**Output phages**	**Output input**	**Input phages**	**Output phages**	**Output input**
100 nanoM peptide	1.2×10^{11}	1.8×10^{10}	1.5×10^{-1}	1.0×10^{11}	5.0×10^{10}	5.0×10^{-1}
hCAT1 cells (k08)	9.8×10^{11}	1.1×10^{6}	1.1×10^{-6}	1.1×10^{12}	7.2×10^{8}	6.5×10^{-4}
hCAT1 cells (k08)	ND	2×10^{4}	-			
hCAT1 cells (k08)	2.6×10^{10}	2.1×10^{5}	8.1×10^{-6}			

Table 2

Round	Target	Insert sequence	No of identical clones
Amplified library	None	EQSRPSWQLTPT	1
		QTHQLLRKPPSF	1
		YMHEPITPNPVT	1
		WHHIPNSAKISL	1
		SENLTLMTVLQM	1
		NLMPPPVPRLPL	1
		TPQGVHYHPNMR	1
1	hCAT1 peptide	ND	
2	hCAT1 peptide	ND	
3	hCAT1 peptide	TLNNHTTPPAWN	1
		QVVHSPFPTSRP	1
4	hCAT1 peptide	ND	
5	hCAT1 peptide	FEQHNWWDSHPQ	1
		NTFDLWLQSVPQ	7
6	hCAT1 peptide	FEGCHPQSGLSC	1
		FEQHNWWDSHPQ	1
		NTFDLWLQSVPQ	5
		SVSVGMKPSPRP	4
1	HCAT1 cells	SVSVGMKPSPRP	4
2	hCAT1 cells	SVSVGMKPSPRP	4
3	hCAT1 cells	SVSVGMKPSPRP	23

Table 3

Binding and internalisation of phages displaying peptide SVSVGMKP-SPRP				
Cell-line:	**Temp:**	**Phage rescue:**	**#pfu x 1000:**	
			clone #26	**12-mer library**
911-hCAT1	37C	Elution	120	4.32
		Lysis	72	18.72
911-hCAT1	37C	Whole sample lysis	205.2	88.2
911-pcDNA3	37C	Elution	55.68	3.84
		Lysis	47.52	8.64
911-pcDNA3	37C	Whole sample lysis	216	0

Table 4

Selection	**Input phages**	**output phages**	**Output/input ratio**
500 nanoM peptide	2.7×10^{12}	9.0×10^{5}	3.6×10^{-7}
500 nanoM peptide	5.7×10^{12}	2.0×10^{6}	3.3×10^{-7}
100 nanoM peptide	9.5×10^{12}	1.5×10^{10}	1.6×10^{-3}
20 nanoM peptide	7.0×10^{12}	3.7×10^{10}	5.2×10^{-3}
hCAT1 cells (k08)	7.0×10^{12}	3.0×10^{6}	4.4×10^{-7}
hCAT1 cells (k08)	5.4×10^{12}	1.7×10^{7}	3.1×10^{-6}
hCAT1 cells (k08)	5.4×10^{12}	1.5×10^{7}	2.8×10^{-6}

Table 5a.
Insertion of hCAT1 binding peptides in LTSLTP or PFSS site of ecotropic murine leukemia envelope.

Sequence (5'-...-3')	Description	Name 2
ttgagcagcataattggtgggattcgcatcctcagccccgggcccccttgt	FEQHNWWDSHPQ at PFSS	Pepenv01 Sense
ctgaggatgcgaatcccaccaccaattatgctgctcaaaggattgatattctagccc	FEQHNWWDSHPQ at PFSS	Pepenv02 Anti
tttgagcagcataattggtgggattcgcatcctcagcggtgcaacactgcctgg	FEQHNWWDSHPQ at LTSLTP	Pepenv03 Sense
ctgaggatgcgaatcccaccaattatgctgctcaaaaggttcttcgcagtctct	FEQHNWWDSHPQ at LTSLTP	Pepenv04 Anti
aatacttttgatctttggctgcagtctgttcctcagccccgggcccccttgt	NTFDLWLQSVPQ at PFSS	Pepenv05 Sense
ctgaggaacagactgcagccaaagatcaaaagtattggattgatattctagccc	NTFDLWLQSVPQ at PFSS	Pepenv06 Anti
aatacttttgatctttggctgcagtctgttcctcagcggtgcaacactgcctgg	NTFDLWLQSVPQ at LTSLTP	Pepenv07 Sense
ctgaggaacagactgcagccaaagatcaaaagtattaggttcttcgcagtctct	NTFDLWLQSVPQ at LTSLTP	Pepenv08 Anti
tctgttctgtgggtatgaagccgagtcctaggcctcccccgggcccccttgt	SVSVGMKPSPRP at PFSS	Pepenv09 Sense
aggcctaggactcggcttcatacccacagaaacagaggattgatattctagccc	SVSVGMKPSPRP at PFSS	Pepenv10 Anti
tctgttctgtgggtatgaagccgagtcctaggcctcggtgcaacactgcctgg	SVSVGMKPSPRP at LTSLTP	Pepenv11 Sense
aggcctaggactcggcttcatacccacagaaacagaaggttcttcgcagtctct	SVSVGMKPSPRP at LTSLTP	Pepenv12 Anti
tttgagggtgtcatcctcagtcgggctgtcttgtccccgggggcccccttgt	FEGCHPQSGLSC at PFSS	Pepenv13 Sense
acaagacagccccgactgaggatgacacccctcaaaggattgatattctagccc	FEGCHPQSGLSC at PFSS	Pepenv14 Anti
tttgagggtgtcatcctcagtcgggctgtcttgtcggtgcaacactgcctgg	FEGCHPQSGLSC at LTSLTP	Pepenv15 Sense
acaagacagccccgactgaggatgacacccctcaaaaggttcttcgcagtctct	FEGCHPQSGLSC at LTSLTP	Pepenv16 Anti

Table 5b.
Insertion of hCAT1 binding peptides in BstEII site of ecotropic murine leukemia envelope.
Underlined sequences of peptide inserts indicate linker amino acid residues.

Sequence (5'-....-3')	Peptide insert	Name 2
atcacctgggaggtaaccggccatatgtttgagcagcataattggtgggattcg catccctcagggtgctagcttggtaaccaatggagatcg	GHMFEQHNWWDSHPQGASLVT	Pepenv17 Sense
cgatctccattggttaccaagctagcaccctgaggatgcgaatcccaccaatta tgctgctcaaacatatggccggttacctcccaggtgat	GHMFEQHNWWDSHPQGASLVT	Pepenv18 Anti
atcacctgggaggtaaccggccatatgaatacttttgatctttggctgcagtcct gttcctcagggtgctagcttggtaaccaatggagatcg	GHMNTFDLWLQSVPQGASLVT	Pepenv19 Sense
cgatctccattggttaccaagctagcaccctgaggaacagactgcagccaaaga tcaaaagtattccatatggccggttacctcccaggtgat	GHMNTFDLWLQSVPQGASLVT	Pepenv20 Anti
atcacctgggaggtaaccggccatatgtctgttctgtgggtatgaagccgagt cctaggcctggtgctagcttggtaaccaatggagatcg	GHMSVSVGMKPSPRPGASLVT	Pepenv21 Sense
cgatctccattggttaccaagctagcaccaggcctaggactcggcttcataccc acagaaacagacatatggccggttacctcccaggtgat	GHMSVSVGMKPSPRPGASLVT	Pepenv22 Anti
atcacctgggaggtaaccggccatatgtttgaggggtgtcatcctcagtcgggg ctgtcttgtggtgctagcttggtaaccaatggagatcg	GHMFEGCHPQSGLSCGASLVT	Pepenv23 Sense
cgatctccattggttaccaagctagcaccacaagacagccccgactgaggatga caccctcaaacatatggccggttacctcccaggtgat	GHMFEGCHPQSGLSCGASLVT	Pepenv24 Anti

Table 5c.
Primers for construction of gpIII/env2 with peptide insertions and to determine insert and orientation of hCAT1 peptide insertions BstEII site of ecotropic murine leukemia envelope.

Peptide insertion	**Name**	**Strand**	**Sequence (5'-....-3')**
FEQHNWWDSHPQ	Pepenv25	Sense	tgagcagcataattggtggg
NTFDLWLQSVPQ	Pepenv26	Sense	ttgatctttggctgcagtct
SVSVGMKPSPRP	Pepenv27	Sense	tctgtgggtatgaagccgag
FEGCHPQSGLSC	Pepenv28	Sense	tttgaggggtgtcatcctca
Priming site	**Name**	**Strand**	**Sequence**
3' of PinA1 site in ecotropic envelope	Ecoenv05	Antisense	gtcctagattttggtatctg
Fusion envelope and pelB leader sequence protein m13, NotI site	Ecoenv17	Sense	ctcgctcgcccatatgcggccgcaggtcctcctcttagcagcacaacc agcaatggccgcttcgcccggctcc
Fusion envelope and gIII protein m13, SpeI and SgrA1 site	Ecoenv12	Antisense	agcatcactagtcgccggtggaagttg

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:
(A) NAME: Introgene B.V.
(B) STREET: Wassenaarseweg 72
(C) CITY: Leiden
(D) STATE: Zuid-Holland
(E) COUNTRY: the Netherlands
(F) POSTAL CODE (ZIP): 2333 AL

(ii) TITLE OF INVENTION: Targeted delivery through a cationic amino acid transporter.

(iii) NUMBER OF SEQUENCES: 59

(iv) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

(v) CURRENT APPLICATION DATA:
APPLICATION NUMBER: EP 98201693.3

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

Lys Asn Trp Gln Leu Thr Glu Glu Asp Phe Gly Asn Thr Ser Gly Arg
1 5 10 15

Leu Cys Leu Asn Asn Asp Thr Lys Glu Gly Lys Pro Gly Val Gly Gly
20 25 30

Phe

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

CCCTCATAGT TAGCGTAACG
20

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

Ser Val Ser Val Gly Met Lys Pro Ser Pro Arg Pro
1 5 10

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Glu Gln Ser Arg Pro Ser Trp Gln Leu Thr Pro Thr
1 5 10

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

Gln Thr His Gln Leu Leu Arg Lys Pro Pro Ser Phe

1 5 10

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Tyr Met His Glu Pro Ile Thr Pro Asn Pro Val Thr
1 5 10

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

Trp His His Ile Pro Asn Ser Ala Lys Ile Ser Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Ser Glu Asn Leu Thr Leu Met Thr Val Leu Gln Met
1 5 10

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

Asn Leu Met Pro Pro Pro Val Pro Arg Leu Pro Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Thr Pro Gln Gly Val His Tyr His Pro Asx Asn Met Arg
1 5 10

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

Thr Leu Asn Asn His Thr Thr Pro Pro Ala Trp Asn
1 5 10

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

Gln Val Val His Ser Pro Phe Pro Thr Ser Arg Pro
1 5 10

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

Phe Glu Gln His Asn Trp Trp Asp Ser His Pro Gln
1 5 10

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

Asn Thr Phe Asp Leu Trp Leu Gln Ser Val Pro Gln
1 5 10

(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

Phe Glu Gly Cys His Pro Gln Ser Gly Leu Ser Cys
1 5 10

(2) INFORMATION FOR SEQ ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

TTTGAGCAGC ATAATTGGTG GGATTCGCAT CCTCAGCCCC CGGGGCCCCC TTGT
54

(2) INFORMATION FOR SEQ ID NO: 17:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

CTGAGGATGC GAATCCCACC AATTATGCTG CTCAAAGGAT TGATATTCTA GCCC
54

(2) INFORMATION FOR SEQ ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

TTTGAGCAGC ATAATTGGTG GGATTCGCAT CCTCAGCGGT GCAACACTGC CTGG
54

(2) INFORMATION FOR SEQ ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

CTGAGGATGC GAATCCCACC AATTATGCTG CTCAAAAGGT TCTTCGCAGT CTCT
54

(2) INFORMATION FOR SEQ ID NO: 20:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

AATACTTTTG ATCTTTGGCT GCAGTCTGTT CCTCAGCCCC CGGGGCCCCC TTGT
54

(2) INFORMATION FOR SEQ ID NO: 21:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

CTGAGGAACA GACTGCAGCC AAAGATCAAA AGTATTGGAT TGATATTCTA GCCC
54

(2) INFORMATION FOR SEQ ID NO: 22:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

AATACTTTTG ATCTTTGGCT GCAGTCTGTT CCTCAGCGGT GCAACACTGC CTGG
54

(2) INFORMATION FOR SEQ ID NO: 23:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

CTGAGGAACA GACTGCAGCC AAAGATCAAA AGTATTAGGT TCTTCGCAGT CTCT
54

(2) INFORMATION FOR SEQ ID NO: 24:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

TCTGTTTCTG TGGGTATGAA GCCGAGTCCT AGGCCTCCCC CGGGGCCCCC TTGT
54

(2) INFORMATION FOR SEQ ID NO: 25:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

AGGCCTAGGA CTCGGCTTCA TACCCACAGA AACAGAGGAT TGATATTCTA GCCC
54

(2) INFORMATION FOR SEQ ID NO: 26:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

TCTGTTTCTG TGGGTATGAA GCCGAGTCCT AGGCCTCGGT GCAACACTGC CTGG
54

(2) INFORMATION FOR SEQ ID NO: 27:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

AGGCCTAGGA CTCGGCTTCA TACCCACAGA AACAGAAGGT TCTTCGCAGT CTCT
54

(2) INFORMATION FOR SEQ ID NO: 28:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

TTTGAGGGGT GTCATCCTCA GTCGGGGCTG TCTTGTCCCC CGGGGCCCCC TTGT
54

(2) INFORMATION FOR SEQ ID NO: 29:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

ACAAGACAGC CCCGACTGAG GATGACACCC CTCAAAGGAT TGATATTCTA GCCC
54

(2) INFORMATION FOR SEQ ID NO: 30:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

TTTGAGGGGT GTCATCCTCA GTCGGGGCTG TCTTGTCGGT GCAACACTGC CTGG
54

(2) INFORMATION FOR SEQ ID NO: 31:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

ACAAGACAGC CCCGACTGAG GATGACACCC CTCAAAAGGT TCTTCGCAGT CTCT
54

(2) INFORMATION FOR SEQ ID NO: 32:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 92 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: unknown

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

ATCACCTGGG AGGTAACCGG CCATATGTTT GAGCAGCATA ATTGGTGGGA TTCGCATCCT
60

CAGGGTGCTA GCTTGGTAAC CAATGGAGAT CG
92

(2) INFORMATION FOR SEQ ID NO: 33:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 92 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

CGATCTCCAT TGGTTACCAA GCTAGCACCC TGAGGATGCG AATCCCACCA ATTATGCTGC
60

TCAAACATAT GGCCGGTTAC CTCCCAGGTG AT
92

(2) INFORMATION FOR SEQ ID NO: 34:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 92 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

ATCACCTGGG AGGTAACCGG CCATATGAAT ACTTTTGATC TTTGGCTGCA GTCTGTTCCT
60

CAGGGTGCTA GCTTGGTAAC CAATGGAGAT CG
92

(2) INFORMATION FOR SEQ ID NO: 35:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 92 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

CGATCTCCAT TGGTTACCAA GCTAGCACCC TGAGGAACAG ACTGCAGCCA AAGATCAAAA
60

GTATTCATAT GGCCGGTTAC CTCCCAGGTG AT
92

(2) INFORMATION FOR SEQ ID NO: 36:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 92 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

ATCACCTGGG AGGTAACCGG CCATATGTCT GTTTCTGTGG GTATGAAGCC GAGTCCTAGG
60

CCTGGTGCTA GCTTGGTAAC CAATGGAGAT CG
92

(2) INFORMATION FOR SEQ ID NO: 37:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 92 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

CGATCTCCAT TGGTTACCAA GCTAGCACCA GGCCTAGGAC TCGGCTTCAT ACCCACAGAA
60

ACAGACATAT GGCCGGTTAC CTCCCAGGTG AT
92

(2) INFORMATION FOR SEQ ID NO: 38:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 92 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

ATCACCTGGG AGGTAACCGG CCATATGTTT GAGGGGTGTC ATCCTCAGTC GGGGCTGTCT
60

TGTGGTGCTA GCTTGGTAAC CAATGGAGAT CG
92

(2) INFORMATION FOR SEQ ID NO: 39:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 92 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

CGATCTCCAT TGGTTACCAA GCTAGCACCA CAAGACAGCC CCGACTGAGG ATGACACCCC
60

TCAAACATAT GGCCGGTTAC CTCCCAGGTG AT
92

(2) INFORMATION FOR SEQ ID NO: 40:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

Gly His Met Phe Glu Gln His Asn Trp Trp Asp Ser His Pro Gln Gly
1 5 10 15

Ala Ser Leu Val Thr
20

(2) INFORMATION FOR SEQ ID NO: 41:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

Gly His Met Asn Thr Phe Asp Leu Trp Leu Gln Ser Val Pro Gln Gly
1 5 10 15

Ala Ser Leu Val Thr
20

(2) INFORMATION FOR SEQ ID NO: 42:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

Gly His Met Ser Val Ser Val Gly Met Lys Pro Ser Pro Arg Pro Gly
1 5 10 15

Ala Ser Leu Val Thr
20

(2) INFORMATION FOR SEQ ID NO: 43:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

Gly His Met Phe Glu Gly Cys His Pro Gln Ser Gly Leu Ser Cys Gly
1 5 10 15

Ala Ser Leu Val Thr
20

(2) INFORMATION FOR SEQ ID NO: 44:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

TGAGCAGCAT AATTGGTGGG
20

(2) INFORMATION FOR SEQ ID NO: 45:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

TTGATCTTTG GCTGCAGTCT
20

(2) INFORMATION FOR SEQ ID NO: 46:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

TCTGTGGGTA TGAAGCCGAG
20

(2) INFORMATION FOR SEQ ID NO: 47:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

TTTGAGGGGT GTCATCCTCA
20

(2) INFORMATION FOR SEQ ID NO: 48:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

GTCCTAGATT TTGGTATCTG
20

(2) INFORMATION FOR SEQ ID NO: 49:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 75 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

CTCGCTCGCC CATATGCGGC CGCAGGTCTC CTCCTCTTAG CAGCACAACC AGCAATGGCC
60

GCTTCGCCCG GCTCC
75

(2) INFORMATION FOR SEQ ID NO: 50:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

AGCATCACTA GTCGCCGGTG GAAGTTG
27

(2) INFORMATION FOR SEQ ID NO: 51:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

AAAAACTGGC AGCTCACGGA GGAGGATTTT GGGAACACAT CAGGCCGTCT C
51

(2) INFORMATION FOR SEQ ID NO: 52:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

Lys Asn Trp Gln Leu Thr Glu Glu Asp Phe Gly Asn Thr Ser Gly Arg
1 5 10 15

Leu

(2) INFORMATION FOR SEQ ID NO: 53:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 48 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: unknown

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

TGTTTGAACA ATGACACAAA AGAAGGGAAG CCCGGTGTTG GTGGATTC
48

(2) INFORMATION FOR SEQ ID NO: 54:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

Cys Leu Asn Asn Asp Thr Lys Glu Gly Lys Pro Gly Val Gly Gly Phe
1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 55:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

Lys Arg Arg Asn Asn Asp Thr Lys Glu Gly Lys Pro Gly Val Gly Gly
1 5 10 15

Phe Met Pro Phe Gly Phe Ser Gly Val Leu Ser
20 25

(2) INFORMATION FOR SEQ ID NO: 56:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56:

Lys Arg Arg Asn Asn Asp Thr Asn Val Lys Tyr Gly Glu Gly Gly Phe
1 5 10 15

Met Pro Phe Gly Phe Ser Gly Val Leu Ser
20 25

(2) INFORMATION FOR SEQ ID NO: 57:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5925 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

GACGAAAGGG CCTCGTGATA CGCCTATTTT TATAGGTTAA TGTCATGATA ATAATGGTTT
60

CTTAGACGTC AGGTGGCACT TTTCGGGGAA ATGTGCGCGG AACCCCTATT TGTTTATTTT
120

TCTAAATACA TTCAAATATG TATCCGCTCA TGAGACAATA ACCCTGATAA ATGCTTCAAT
180

AATATTGAAA AAGGAAGAGT ATGAGTATTC AACATTTCCG TGTCGCCCTT ATTCCCTTTT
240

TTGCGGCATT TTGCCTTCCT GTTTTTGCTC ACCCAGAAAC GCTGGTGAAA GTAAAAGATG
300

CTGAAGATCA GTTGGGTGCC CGAGTGGGTT ACATCGAACT GGATCTCAAC AGCGGTAAGA
360

TCCTTGAGAG TTTTCGCCCC GAAGAACGTT TTCCAATGAT GAGCACTTTT AAAGTTCTGC
420

TATGTGGCGC GGTATTATCC CGTATTGACG CCGGGCAAGA GCAACTCGGT CGCCGCATAC
480

ACTATTCTCA GAATGACTTG GTTGAGTACT CACCAGTCAC AGAAAAGCAT CTTACGGATG
540

GCATGACAGT AAGAGAATTA TGCAGTGCTG CCATAACCAT GAGTGATAAC ACTGCGGCCA
600

ACTTACTTCT GACAACGATC GGAGGACCGA AGGAGCTAAC CGCTTTTTTG CACAACATGG
660

GGGATCATGT AACTCGCCTT GATCGTTGGG AACCGGAGCT GAATGAAGCC ATACCAAACG

720

ACGAGCGTGA CACCACGATG CCTGTAGCAA TGGCAACAAC GTTGCGCAAA CTATTAACTG
780

GCGAACTACT TACTCTAGCT TCCCGGCAAC AATTAATAGA CTGGATGGAG GCGGATAAAG
840

TTGCAGGACC ACTTCTGCGC TCGGCCCTTC CGGCTGGCTG GTTTATTGCT GATAAATCTG
900

GAGCCGGTGA GCGTGGGTCT CGCGGTATCA TTGCAGCACT GGGGCCAGAT GGTAAGCCCT
960

CCCGTATCGT AGTTATCTAC ACGACGGGGA GTCAGGCAAC TATGGATGAA CGAAATAGAC
1020

AGATCGCTGA GATAGGTGCC TCACTGATTA AGCATTGGTA ACTGTCAGAC CAAGTTTACT
1080

CATATATACT TTAGATTGAT TTAAAACTTC ATTTTTAATT TAAAAGGATC TAGGTGAAGA
1140

TCCTTTTTGA TAATCTCATG ACCAAAATCC CTTAACGTGA GTTTTCGTTC CACTGAGCGT
1200

CAGACCCCGT AGAAAAGATC AAAGGATCTT CTTGAGATCC TTTTTTTCTG CGCGTAATCT
1260

GCTGCTTGCA AACAAAAAAA CCACCGCTAC CAGCGGTGGT TTGTTTGCCG GATCAAGAGC
1320

TACCAACTCT TTTTCCGAAG GTAACTGGCT TCAGCAGAGC GCAGATACCA AATACTGTCC
1380

TTCTAGTGTA GCCGTAGTTA GGCCACCACT TCAAGAACTC TGTAGCACCG CCTACATACC
1440

TCGCTCTGCT AATCCTGTTA CCAGTGGCTG CTGCCAGTGG CGATAAGTCG TGTCTTACCG
1500

GGTTGGACTC AAGACGATAG TTACCGGATA AGGCGCAGCG GTCGGGCTGA ACGGGGGGTT
1560

CGTGCATACA GCCCAGCTTG GAGCGAACGA CCTACACCGA ACTGAGATAC CTACAGCGTG
1620

AGCATTGAGA AAGCGCCACG CTTCCCGAAG GGAGAAAGGC GGACAGGTAT CCGGTAAGCG
1680

GCAGGGTCGG AACAGGAGAG CGCACGAGGG AGCTTCCAGG GGGAAACGCC TGGTATCTTT
1740

ATAGTCCTGT CGGGTTTCGC CACCTCTGAC TTGAGCGTCG ATTTTTGTGA TGCTCGTCAG
1800

GGGGGCGGAG CCTATGGAAA AACGCCAGCA ACGCGGCCTT TTTACGGTTC CTGGCCTTTT
1860

GCTGGCCTTT TGCTCACATG TTCTTTCCTG CGTTATCCCC TGATTCTGTG GATAACCGTA
1920

TTACCGCCTT TGAGTGAGCT GATACCGCTC GCCGCAGCCG AACGACCGAG CGCAGCGAGT
1980

CAGTGAGCGA GGAAGCGGAA GAGCGCCCAA TACGCAAACC GCCTCTCCCC GCGCGTTGGC

2040

CGATTCATTA ATGCAGCTGG CACGACAGGT TTCCCGACTG GAAAGCGGGC AGTGAGCGCA
2100

ACGCAATTAA TGTGAGTTAG CTCACTCATT AGGCACCCCA GGCTTTACAC TTTATGCTTC
2160

CGGCTCGTAT GTTGTGTGGA ATTGTGAGCG GATAACAATT TCACACAGGA AACAGCTATG
2220

ACCATGATTA CGCCAAGCTT TGGAGCCTTT TTTTTGGAGA TTTTCAACGT GAAAAAATTA
2280

TTATTCGCAA TTCCTTTAGT TGTTCCTTTC TATTCTCACA GTGCACTTGA AACGACACTC
2340

ACGCAGTCTC CAGGCATCCT GTCTTTGTCT CCGGGGGCAG GAGCCACCCT CTCCTGCAGG
2400

GCCAGTCAGA GTGTCAGCAG CAGGAACTTA GCCTGGTACC AGCAGAAACC TGGCCAGGCT
2460

CCCAGGCTCC TCATCTATGG TGTATCCAAC AGGGCCACTG GCGTCCCAGA CAGGTTCAGT
2520

GGCAGTGGGT CTGGGGCAGA CTTCACTCTC ACCATCAACA GACTGGAGCC TGAAGATTTT
2580

GCGGTGTATT ACTGTCAGCG GTATGGCAGG TCACTGTGGA CGTTCGGTCA AGGGACCAAG
2640

GTGGAGATCA AACGTGGAAC TGTGGCTGCA CCATCTGTCT TCATCTTCCC GCCATCTGAT
2700

GAGCAGTTGA AATCTGGAAC TGCCTCTGTT GTGTGCCTGC TGAATAACTT CTATCCCAGA
2760

GAGGCCAAAG TACAGTGGAA GGTGGATAAC GCCCTCCAAT CGGGTAACTC CCAGGAGAGT
2820

GTCACAGAGC AGGACAGCAA GGACAGCACC TACAGCCTCA GCAGCACCCT GACGCTGAGC
2880

AAAGCAGACT ACGAGAAACA CAAAGTCTAC GCCTGCGAAG TCACCCATCA GGGCCTGAGT
2940

TCACCGGTGA CAAAGAGCTT CAACAGGGGA GAGTGTTAAT AAGGCGCGCC AATTCTATTT
3000

CAAGGAGACA GTCATAATGA AATACCTATT GCCTACGGCA GCCGCTGGAT TGTTATTACT
3060

CGCGGCCCAG CCGGCCATGG CCCAGGTCCA GCTGGTGCAG TCTGGGGGAG GCGTGGTCCA
3120

GCCTGGGAGG TCCCTGAGAC TCTCCTGTGC AGCCTCTGGA TTCACCTTCA GTAGCTATGC
3180

TATGCACTGG GTCCGCCAGG CTCCAGGCAA GGGGCTGGAG TGGGTGGCAG TTATATCATA
3240

TGATGGAAGC AATAAATACT ACGCAGACTC CGTGAAGGGC CGATTCACCA TCTCCAGAGA
3300

CAATTCCAAG AACACGCTGT ATCTGCAAAT GAACAGCCTG AGAGCTGAGG ACACGGCTGT

3360

GTATTACTGT GCGAGAGGGA TTACAGTAAC TAAATCACGA TTTGACTACT GGGGCCAGGG
3420

CACCCTGGTC ACCGTCTCAA GCGCCTCCAC CAAGGGCCCA TCGGTCTTCC CCCTGGCACC
3480

CTCCTCCAAG AGCACCTCTG GGGGCACAGC GGCCCTGGGC TGCCTGGTCA AGGACTACTT
3540

CCCCGAACCG GTGACGGTGT CGTGGAACTC AGGCGCCCTG ACCAGCGGCG TCCACACCTT
3600

CCCGGCTGTC CTACAGTCCT CAGGACTCTA CTCCCTCAGC AGCGTAGTGA CCGTGCCCTC
3660

CAGCAGCTTG GGCACCCAGA CCTACATCTG CAACGTGAAT CACAAGCCCA GCAACACCAA
3720

GGTGGACAAG AAAGTTGAGC CCAAATCTTG TGCGGCCGCA CATCATCATC ACCATCACGG
3780

GGCCGCAGAA CAAAAACTCA TCTCAGAAGA GGATCTGAAT GGGGCCGCAT AGACTGTTGA
3840

AAGTTGTTTA GCAAAACCTC ATACAGAAAA TTCATTTACT AACGTCTGGA AAGACGACAA
3900

AACTTTAGAT CGTTACGCTA ACTATGAGGG CTGTCTGTGG AATGCTACAG GCGTTGTGGT
3960

TTGTACTGGT GACGAAACTC AGTGTTACGG TACATGGGTT CCTATTGGGC TTGCTATCCC
4020

TGAAAATGAG GGTGGTGGCT CTGAGGGTGG CGGTTCTGAG GGTGGCGGTT CTGAGGGTGG
4080

CGGTACTAAA CCTCCTGAGT ACGGTGATAC ACCTATTCCG GGCTATACTT ATATCAACCC
4140

TCTCGACGGC ACTTATCCGC CTGGTACTGA GCAAAACCCC GCTAATCCTA ATCCTTCTCT
4200

TGAGGAGTCT CAGCCTCTTA ATACTTTCAT GTTTCAGAAT AATAGGTTCC GAAATAGGCA
4260

GGGTGCATTA ACTGTTTATA CGGGCACTGT TACTCAAGGC ACTGACCCCG TTAAAACTTA
4320

TTACCAGTAC ACTCCTGTAT CATCAAAAGC CATGTATGAC GCTTACTGGA ACGGTAAATT
4380

CAGAGACTGC GCTTTCCATT CTGGCTTTAA TGAGGATCCA TTCGTTTGTG AATATCAAGG
4440

CCAATCGTCT GACCTGCCTC AACCTCCTGT CAATGCTGGC GGCGGCTCTG GTGGTGGTTC
4500

TGGTGGCGGC TCTGAGGGTG GCGGCTCTGA GGGTGGCGGT TCTGAGGGTG GCGGCTCTGA
4560

GGGTGGCGGT TCCGGTGGCG GCTCCGGTTC CGGTGATTTT GATTATGAAA AAATGGCAAA
4620

CGCTAATAAG GGGGCTATGA CCGAAAATGC CGATGAAAAC GCGCTACAGT CTGACGCTAA

4680

AGGCAAACTT GATTCTGTCG CTACTGATTA CGGTGCTGCT ATCGATGGTT TCATTGGTGA
4740

CGTTTCCGGC CTTGCTAATG GTAATGGTGC TACTGGTGAT TTTGCTGGCT CTAATTCCCA
4800

AATGGCTCAA GTCGGTGACG GTGATAATTC ACCTTTAATG AATAATTTCC GTCAATATTT
4860

ACCTTCTTTG CCTCAGTCGG TTGAATGTCG CCCTTATGTC TTTGGCGCTG GTAAACCATA
4920

TGAATTTTCT ATTGATTGTG ACAAAATAAA CTTATTCCGT GGTGTCTTTG CGTTTCTTTT
4980

ATATGTTGCC ACCTTTATGT ATGTATTTTC GACGTTTGCT AACATACTGC GTAATAAGGA
5040

GTCTTAATAA GAATTCACTG GCCGTCGTTT TACAACGTCG TGACTGGGAA AACCCTGGCG
5100

TTACCCAACT TAATCGCCTT GCAGCACATC CCCCTTTCGC CAGCTGGCGT AATAGCGAAG
5160

AGGCCCGCAC CGATCGCCCT TCCCAACAGT TGCGCAGCCT GAATGGCGAA TGGCGCCTGA
5220

TGCGGTATTT TCTCCTTACG CATCTGTGCG GTATTTCACA CCGCATATAA ATTGTAAACG
5280

TTAATATTTT GTTAAAATTC GCGTTAAATT TTTGTTAAAT CAGCTCATTT TTTAACCAAT
5340

AGGCCGAAAT CGGCAAAATC CCTTATAAAT CAAAAGAATA GCCCGAGATA GGGTTGAGTG
5400

TTGTTCCAGT TTGGAACAAG AGTCCACTAT TAAAGAACGT GGACTCCAAC GTCAAAGGGC
5460

GAAAAACCGT CTATCAGGGC GATGGCCCAC TACGTGAACC ATCACCCAAA TCAAGTTTTT
5520

TGGGGTCGAG GTGCCGTAAA GCACTAAATC GGAACCCTAA AGGGAGCCCC CGATTTAGAG
5580

CTTGACGGGG AAAGCCGGCG AACGTGGCGA GAAAGGAAGG GAAGAAAGCG AAAGGAGCGG
5640

GCGCTAGGGC GCTGGCAAGT GTAGCGGTCA CGCTGCGCGT AACCACCACA CCCGCCGCGC
5700

TTAATGCGCC GCTACAGGGC GCGTACTATG GTTGCTTTGA CGGGTGCAGT CTCAGTACAA
5760

TCTGCTCTGA TGCCGCATAG TTAAGCCAGC CCCGACACCC GCCAACACCC GCTGACGCGC
5820

CCTGACGGGC TTGTCTGCTC CCGGCATCCG CTTACAGACA AGCTGTGACC GTCTCCGGGA
5880

GCTGCATGTG TCAGAGGTTT TCACCGTCAT CACCGAAACG CGCGA
5925

(2) INFORMATION FOR SEQ ID NO: 58:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 236 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58:

```
Val Lys Lys Leu Leu Phe Ala Ile Pro Leu Val Val Pro Phe Tyr Ser
1               5                  10                  15

His Ser Ala Leu Glu Thr Thr Leu Thr Gln Ser Pro Gly Ile Leu Ser
            20                  25                  30

Leu Ser Pro Gly Ala Gly Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser
        35                  40                  45

Val Ser Ser Arg Asn Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala
    50                  55                  60

Pro Arg Leu Leu Ile Tyr Gly Val Ser Asn Arg Ala Thr Gly Val Pro
65                  70                  75                  80

Asp Arg Phe Ser Gly Ser Gly Ser Gly Ala Asp Phe Thr Leu Thr Ile
                85                  90                  95

Asn Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Arg Tyr
            100                 105                 110

Gly Arg Ser Leu Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
        115                 120                 125

Arg Gly Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
    130                 135                 140

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
145                 150                 155                 160

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
                165                 170                 175

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
            180                 185                 190

Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr
        195                 200                 205

Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser
    210                 215                 220

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225                 230                 235
```

(2) INFORMATION FOR SEQ ID NO: 59:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 254 amino acids
(B) TYPE: amino acid

(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

```
Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Leu Ala
1               5                  10                  15

Ala Gln Pro Ala Met Ala Gln Val Gln Leu Val Gln Ser Gly Gly Gly
            20                  25                  30

Val Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly
        35                  40                  45

Phe Thr Phe Ser Ser Tyr Ala Met His Trp Val Arg Gln Ala Pro Gly
    50                  55                  60

Lys Gly Leu Glu Trp Val Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys
65                  70                  75                  80

Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn
                85                  90                  95

Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp
            100                 105                 110

Thr Ala Val Tyr Tyr Cys Ala Arg Gly Ile Thr Val Thr Lys Ser Arg
        115                 120                 125

Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser
    130                 135                 140

Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr
145                 150                 155                 160

Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro
                165                 170                 175

Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val
            180                 185                 190

His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser
        195                 200                 205

Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile
    210                 215                 220

Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val
225                 230                 235                 240

Glu Pro Lys Ser Cys Ala Ala Ala His His His His His His
                245                 250
```

Claims

1. A virus-like particle or gene delivery vehicle provided with a ligand capable of binding to a human amino acid transporter.

2. A virus-like particle or gene delivery vehicle according to claim 1 for delivery of genes to human cells.

3. A virus-like particle or gene delivery vehicle according to claim 1 or 2 comprising at least one viral protein provided with said ligand.

4. A virus-like particle or gene delivery vehicle according to claim 3 wherein said viral protein comprises an envelope protein.

5. A virus-like particle or gene delivery vehicle according to claim 4 derived from a retrovirus.

6. A virus-like particle or gene delivery vehicle according to claim 3 wherein said viral protein comprises a capsid protein.

7. A virus-like particle or gene delivery vehicle according to claim 6 derived from an adeno virus.

8. A virus-like particle or gene delivery vehicle according to any one of claims 1 to 7 wherein said amino acid transporter is a cationic amino acid transporter.

9. A virus-like particle or gene delivery vehicle according to claim 8 wherein said transporter is a human cationic amino acid transporter-1 (hCAT1).

10. A virus-like particle or gene delivery vehicle according to any one of claims 1 to 9 wherein said ligand comprises an amino acid sequence selected from Table 2, preferably from the last four different sequences of Table 2 or a sequence functionally related thereto.

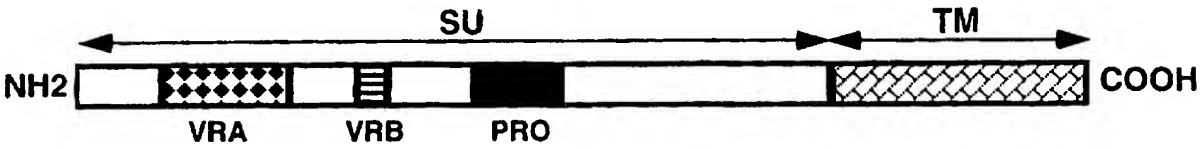
11. A virus-like particle or gene delivery vehicle according to claim 10 wherein said ligand comprises at least a part of the amino acid sequence SVSVGMKPSPRP.

12. A virus-like particle or gene delivery vehicle according to any one of claims 1 to 9 wherein said ligand comprises a fragment derived from a phage displaying at least one antibody fragment selected for its capacity to bind with said amino acid transporter.

13. A virus-like particle or gene delivery vehicle according to claim 12 wherein said antibody fragment comprises an amino acid sequence as shown in Figure 16 or an amino acid sequence functionally equivalent thereto.

Figure 1

Organization of the envelope gene of ecotropic Moloney murine leukemia retrovirus



Env protein processing

Env protein ⟶ SU (gp70) + TM (p15E)

Producer/host cell protease

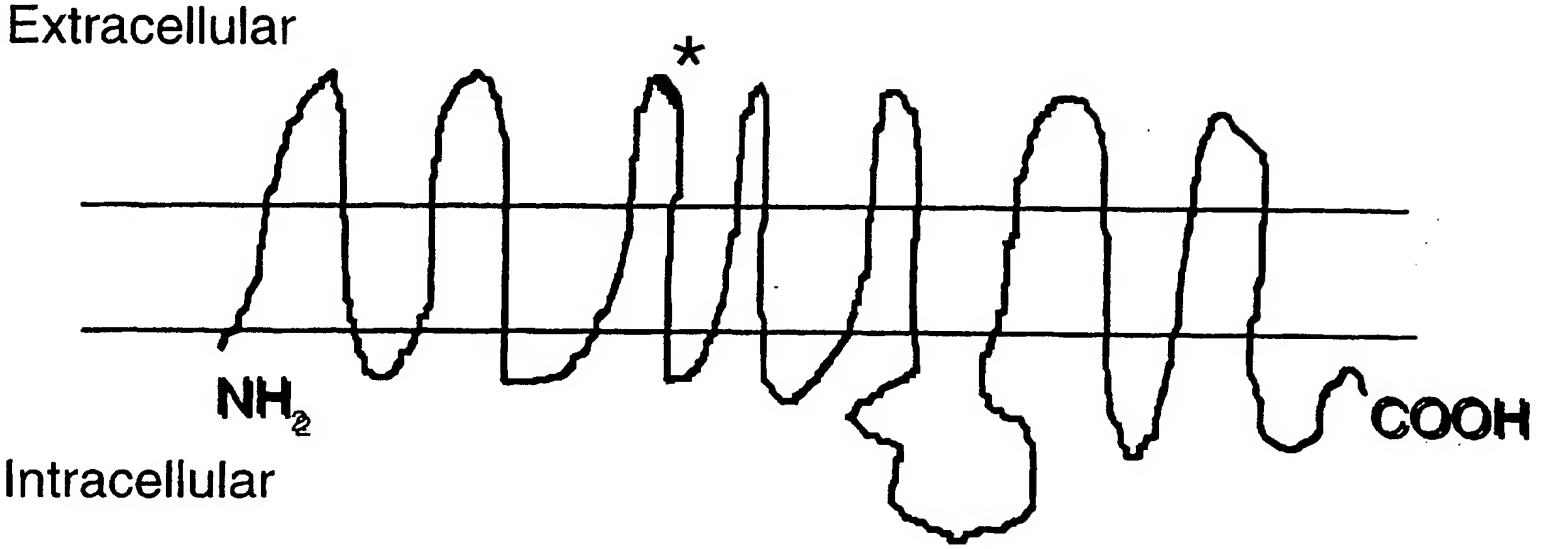
TM(p15E) ⟶ TM(p12E) + R peptide

Viral protease

EP 0 959 136 A1

Figure 2

Theoretical topology CAT-1 receptors in plasmamembrane



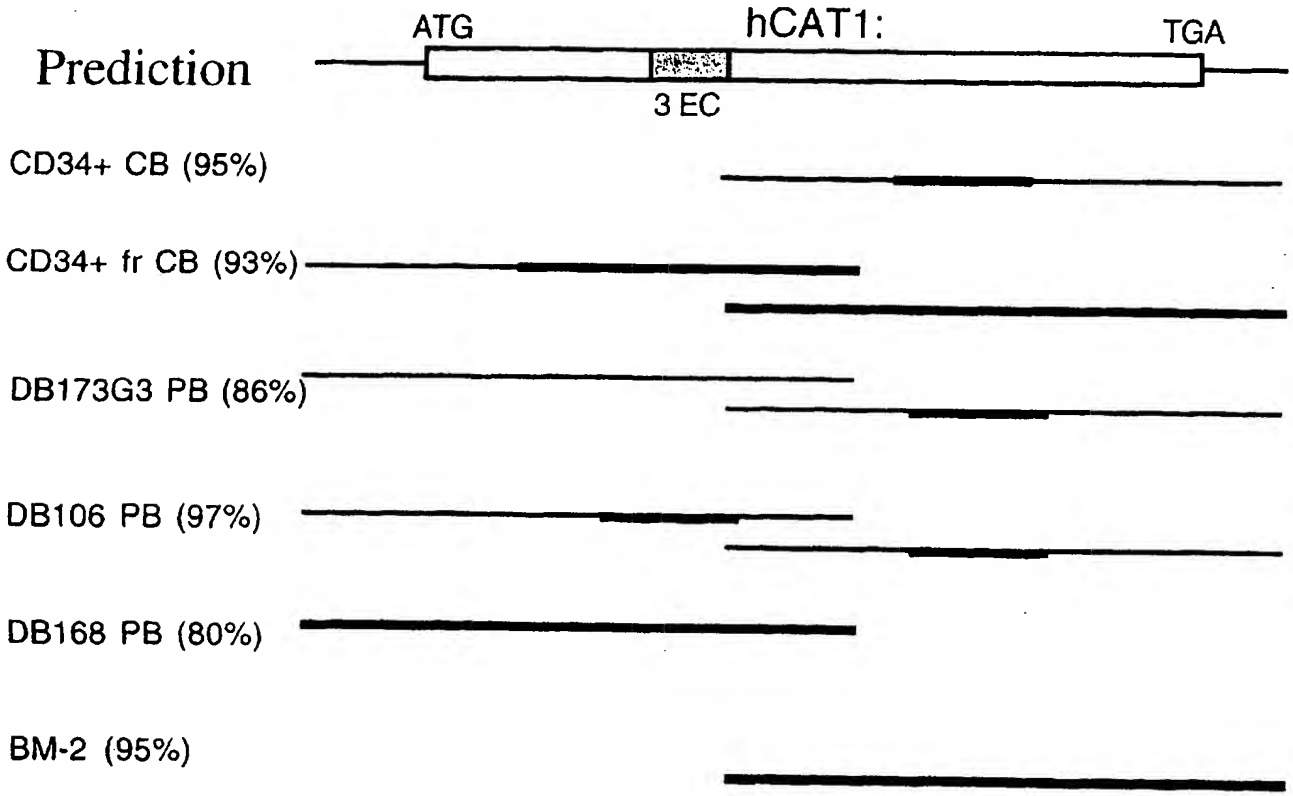
* $YGE_{235-237}$ in mCAT1: permissive for ecotropic virus
  $PGV_{242-244}$ in hCAT1: non-permissive ,,

  $YGE_{235-237}$ in hCAT1: permissive for ecotropic virus
  $PGV_{242-244}$ in mCAT1: non-permissive ,,

EP 0 959 136 A1

Figure 3a

Sequencing hCAT1 cDNA isolated from human CD34+ hemopoietic cells



(%) indicates % $CD34^+$ cells i.e. purity sample used

Figure 3b

Sequencing third extracellular domain hCAT1 cDNA isolated from human CD34+ hemopoietic cells,

1: hCAT1 sequence from human lymphocytes (Yoshimoto et al,1991)
2,3: Sequence of hCAT1 from CD34+ cells isolated from mobilized peripheral blood
3: Sequence of hCAT1 from CD34+ cells isolated from umbillical cord blood

Figure 4

Sequence synthetic hCAT1 and mCAT1 peptides

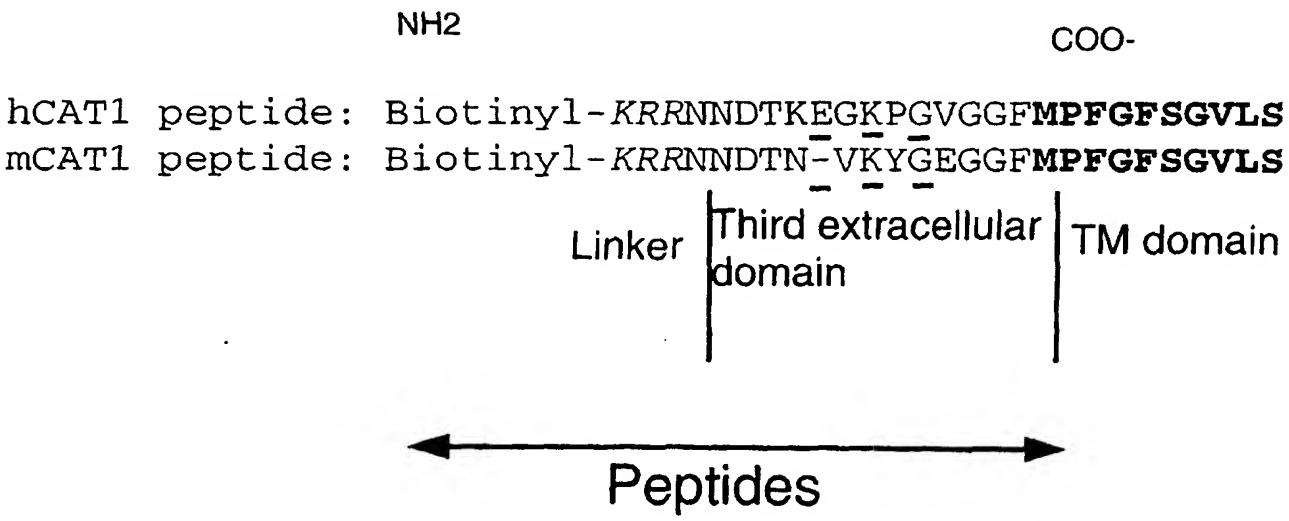


Figure 5

Northern blot analysis of cell lines with hCAT1 probe

1) 911-pcDNA3
2) 911-hCAT1 k08
3) 911
4) 911-hCAT1 pool

Figure 6

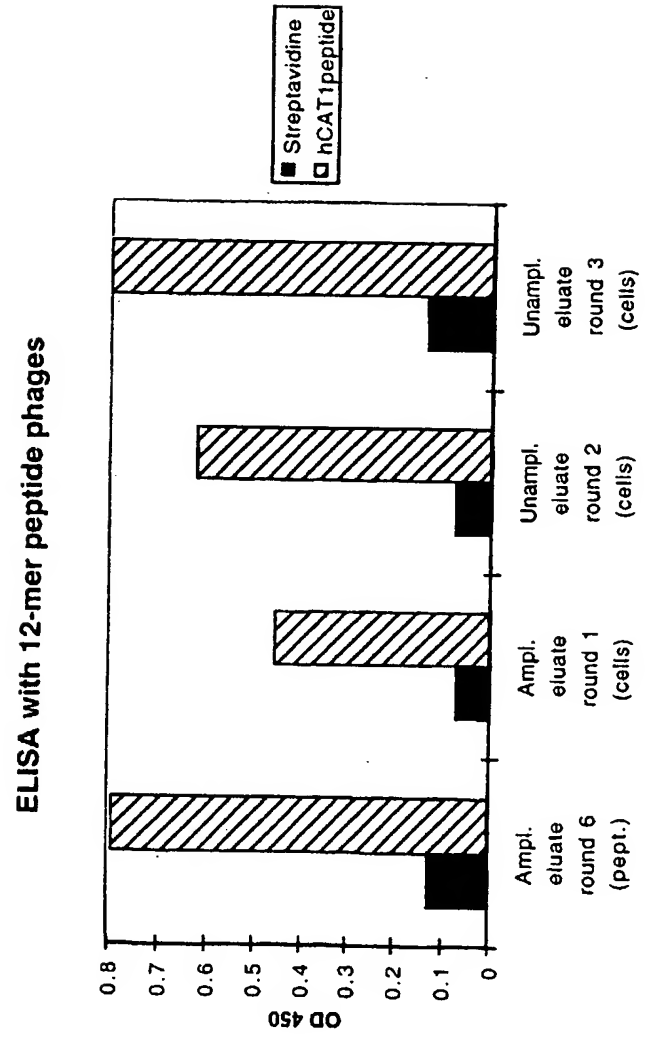

ELISA with 12-mer peptide phages
Streptavidine
hCAT1peptide
OD 450
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0
Ampl. eluate round 6 (pept.)
Ampl. eluate round 1 (cells)
Unampl. eluate round 2 (cells)
Unampl. eluate round 3 (cells)

Figure 7

Binding of cloned 12 mer peptide displaying phages to hCAT1 peptide as measured by ELISA

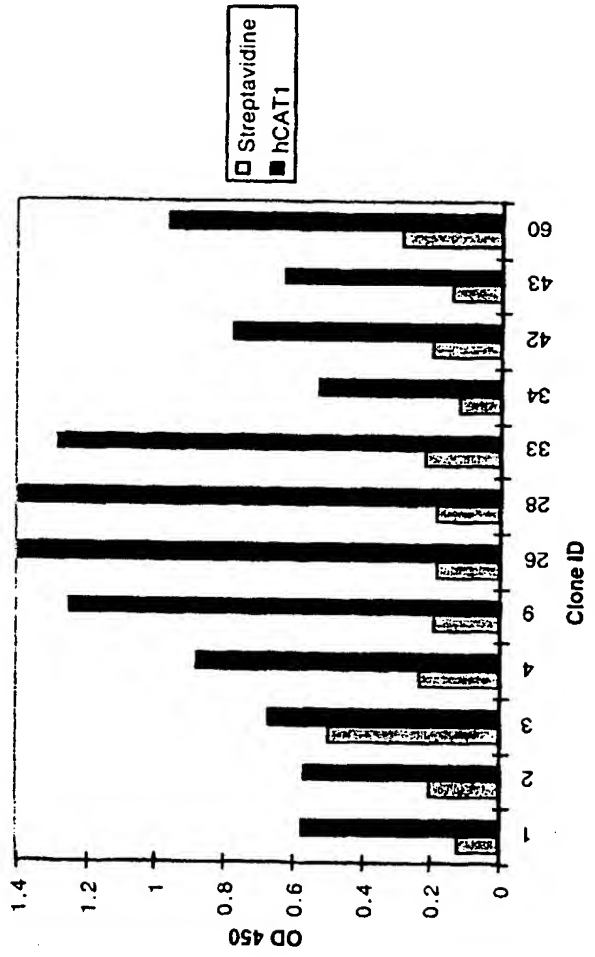


Figure 8

Binding of SVSVGMKPSPRP displaying phage measured by flow cytometry

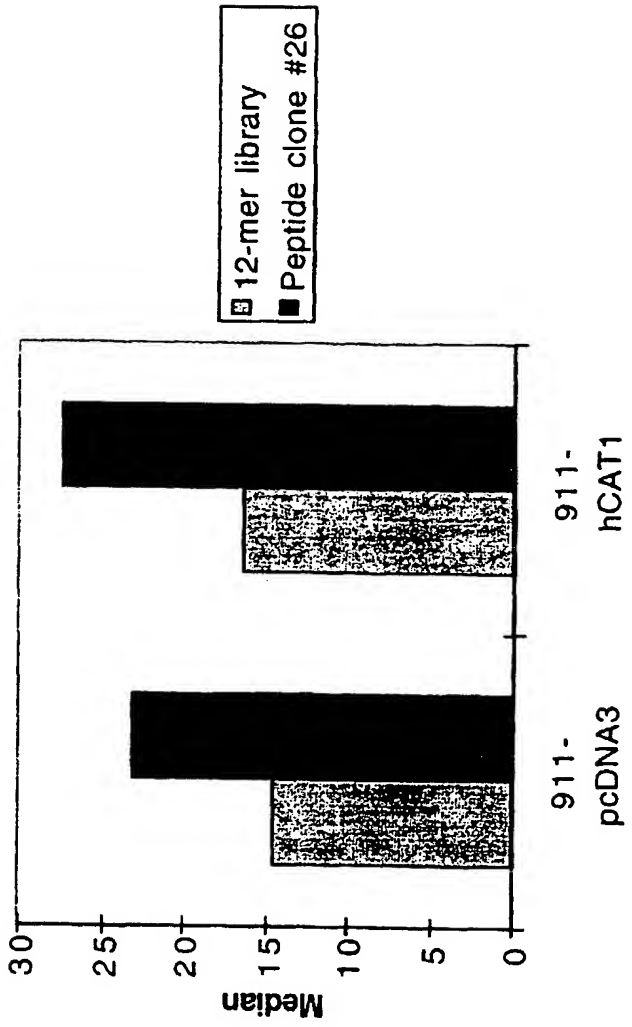


Figure 9

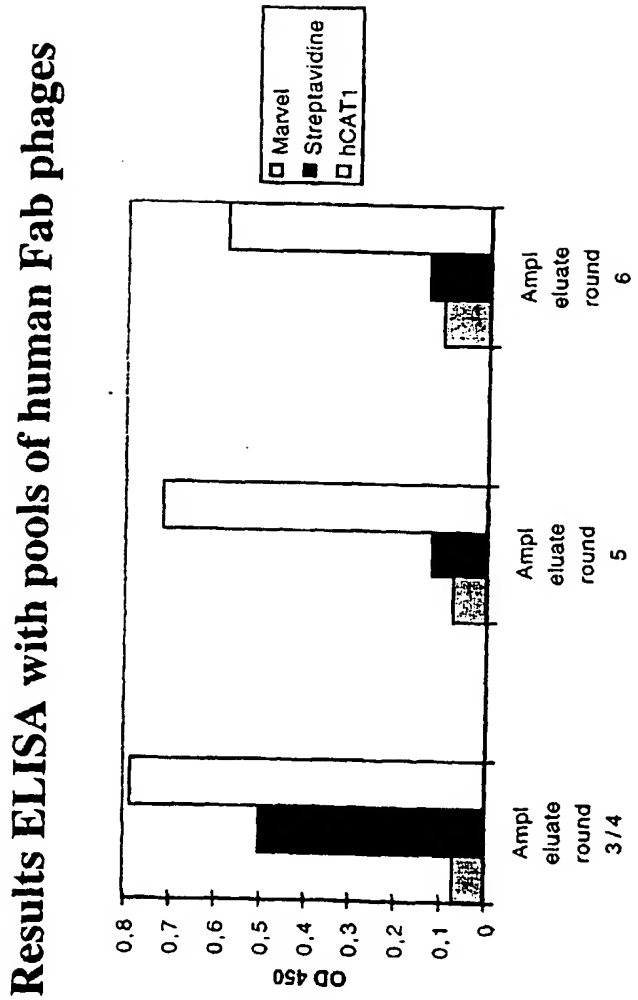

Results ELISA with pools of human Fab phages
Marvel
Streptavidine
hCAT1
OD 450
0,8
0,7
0,6
0,5
0,4
0,3
0,2
0,1
0
Ampl eluate round 3/4
Ampl eluate round 5
Ampl eluate round 6

Figure 10

Binding of human FAb displaying phage pools measured by flow cytometry

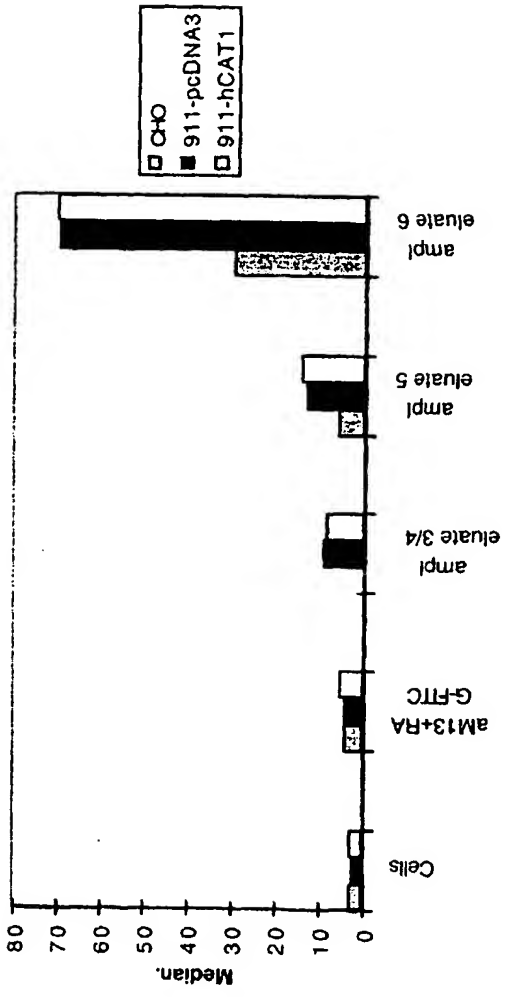


Figure 11

Binding of cloned human FAb displaying phages to hCAT1 peptide as measured by ELISA

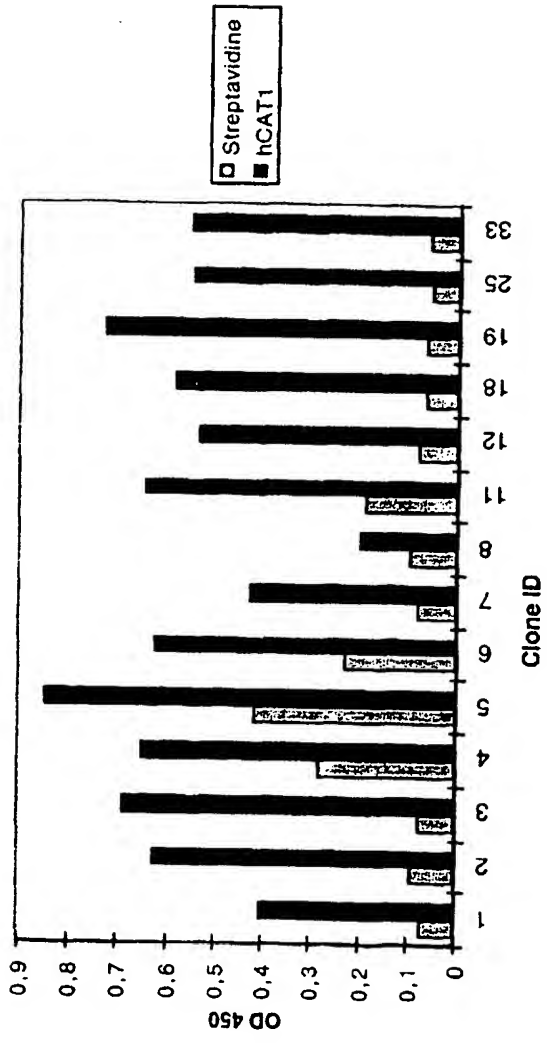


Figure 12

Binding of cloned human FAb displaying phages to hCAT1 expressing cells determined by flow cytometry

Phage:	Median 911-pcDNA	Median 911-hCAT1
	2,27	2,79
	3,62	4,22
1	16,7	13,46
2	21,29	18,27
3	11,44	12,41
4	11,86	8,82
5	12,98	8,82
6	12,3	8,35
7	10,18	8,2
8	17,62	17
11	ND	8,98
12	7,64	12,08
18	11,55	10,84
19	13,1	11,76
25	161,08	151,25
33	11,76	10,27

Figure 13

Example FAb phage clone #25 binding to hCAT1 peptide and hCAT1 expressing unfixed cells

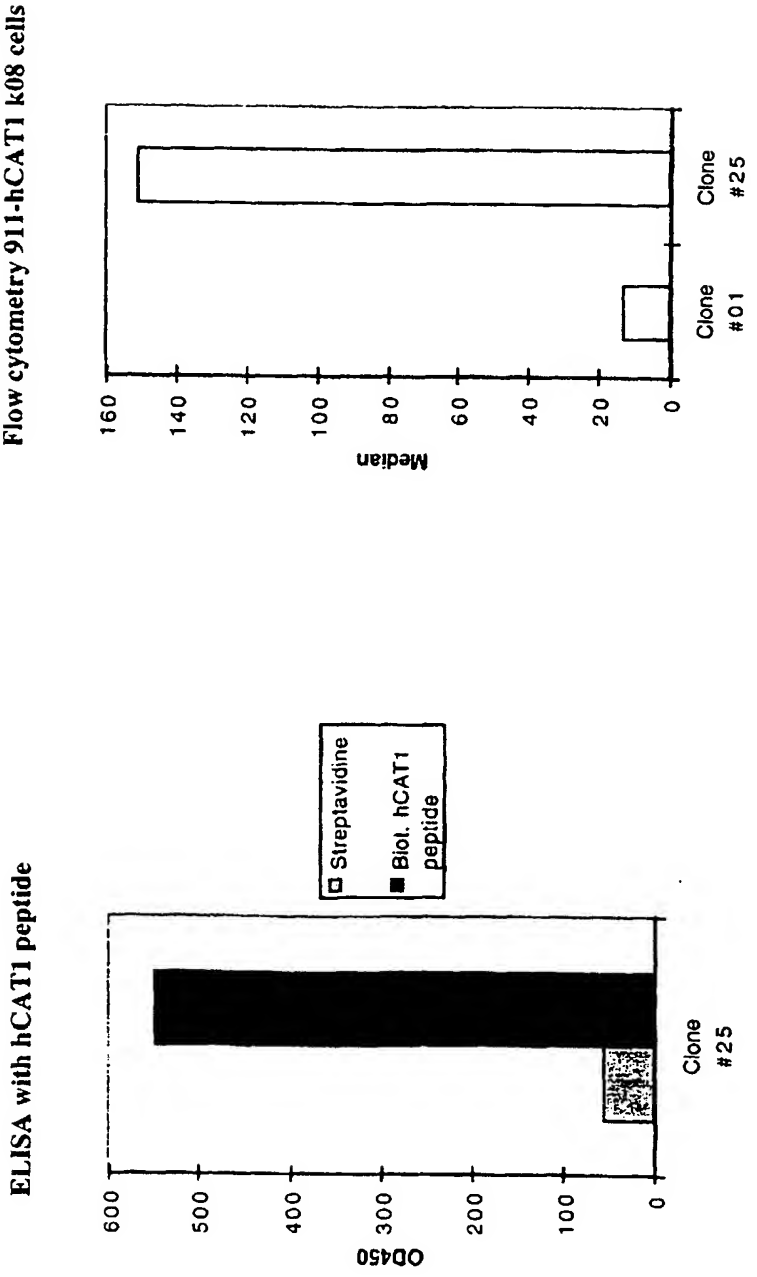
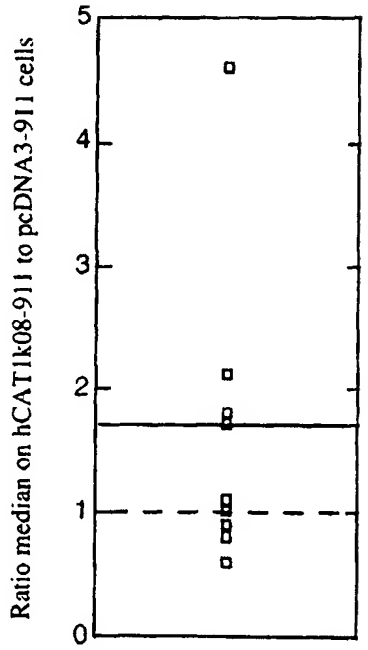


Figure 14

Binding of FAb phage clone #25 to hCAT1 overexpressing cells



Average ratio ± SD :
1.6 ± 1.2 fold, n=10

Figure 15

Vector pCES1 used for construction of human FAb display library

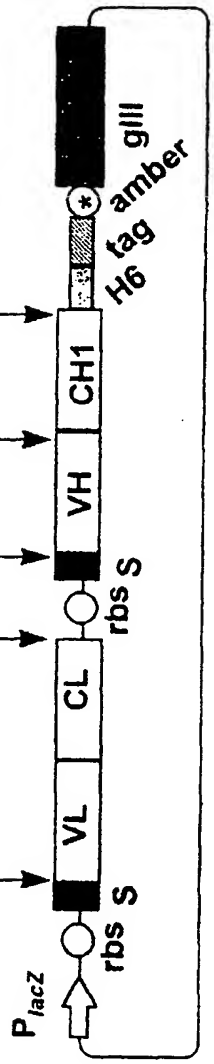
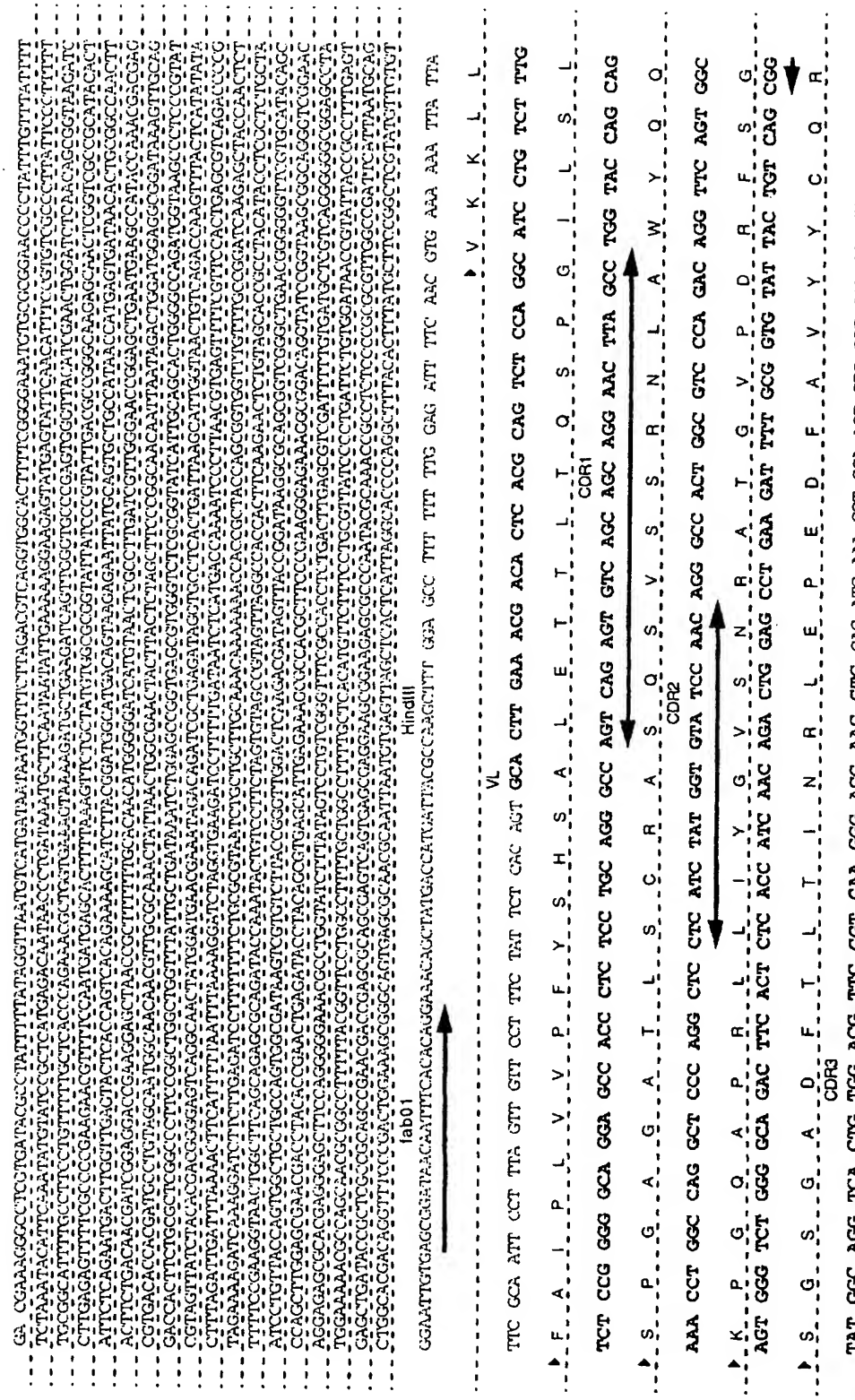
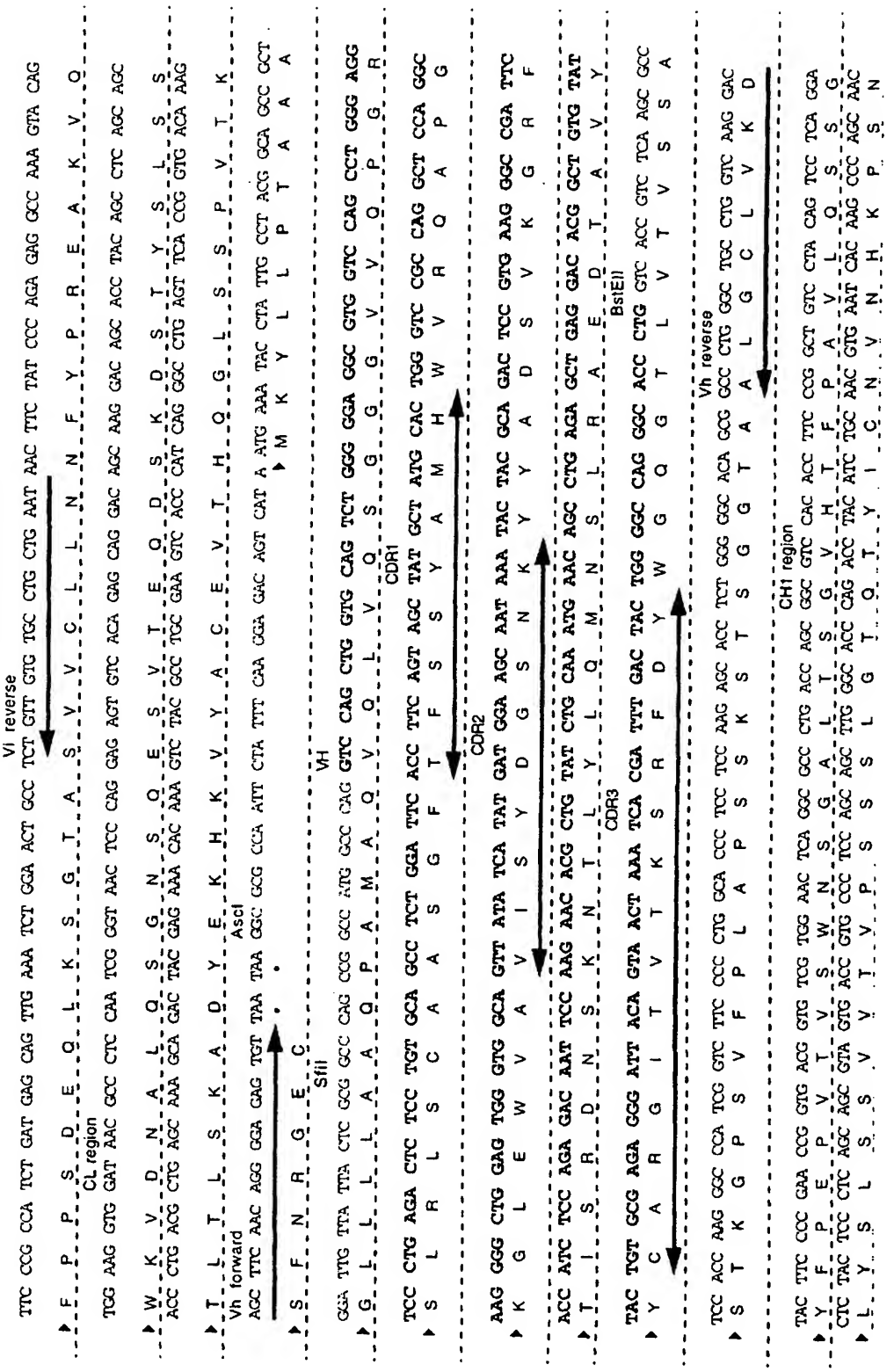


Figure 16

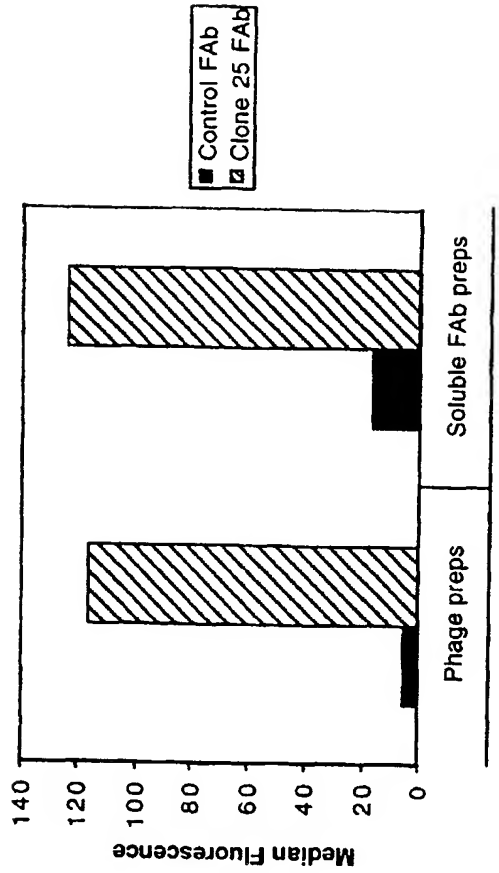
Sequence clone 25


fab01
HindIII
VL
CDR1
CDR2
CDR3


Vl reverse
CL region
Vh forward
AscI
SfiI
VH
CDR1
CDR2
CDR3
BstEII
Vh reverse
CH1 region

NotI
His Tag
fab02

Figure 17
Binding of soluble FAb fragments to hCAT1 expressing cells



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EUROPEAN SEARCH REPORT

Application Number
EP 98 20 1693

DOCUMENTS CONSIDERED TO BE RELEVANT

Category	Citation of document with indication, where appropriate, of relevant passages	Relevant to claim	CLASSIFICATION OF THE APPLICATION (Int.Cl.6)
D,A	ALBRITTON L M ET AL: "A PUTATIVE MURINE ECOTROPIC RETROVIRUS RECEPTOR GENE ENCODES A MULTIPLE MEMBRANE-SPANNING PROTEIN AND CONFERS SUSCEPTIBILITY TO VIRUS INFECTION" CELL, vol. 57, 19 May 1989, pages 659-666, XP002036212 ---	1	C12N15/87 C12N15/86 C12N7/04 C07K16/18
A,D	ALBRITTON, L. M. ET AL.: "Envelope-binding domain in the cationic amino acid transporter determines the host range of ecotropic murine retroviruses" JOURNAL OF VIROLOGY., vol. 67, no. 4, April 1993, pages 2091-2096, XP002084804 ICAN SOCIETY FOR MICROBIOLOGY US * the whole document * ---	1	
A	EP 0 705 844 A (RES DEV FOUNDATION) 10 April 1996 * the whole document * ---	1	
A	US 5 658 782 A (AMARA SUSAN G ET AL) 19 August 1997 * the whole document * ---		TECHNICAL FIELDS SEARCHED (Int.Cl.6) C12N C07K
A	KRASNYKH V N ET AL: "GENERATION OF RECOMBINANT ADENOVIRUS VECTORS WITH MODIFIED FIBERS FOR ALTERING VIRAL TROPISM" JOURNAL OF VIROLOGY, vol. 70, no. 10, October 1996, pages 6839-6846, XP002067518 * the whole document * ---	1	
A	FR 2 649 119 A (CENTRE NAT RECH SCIENT) 4 January 1991 * the whole document * ---	1	
	-/--		

The present search report has been drawn up for all claims

Place of search	Date of completion of the search	Examiner
THE HAGUE	18 November 1998	Chambonnet, F

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L : document cited for other reasons

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DOCUMENTS CONSIDERED TO BE RELEVANT

Category	Citation of document with indication, where appropriate, of relevant passages	Relevant to claim	CLASSIFICATION OF THE APPLICATION (Int.Cl.6)
A	WO 95 26412 A (UAB RESEARCH FOUNDATION) 5 October 1995 * the whole document *	1-5	
A	HONG S S ET AL: "PROTEIN LIGANDS OF THE HUMAN ADENOVIRUS TYPE 2 OUTER CAPSID IDENTIFIED BY BIOPANNING OF A PHAGE-DISPLAYED PEPTIDE LIBRARY ON SEPARATE DOMAINS OF WILD-TYPE AND MUTANT PENTON CAPSOMERS" EMBO JOURNAL, vol. 14, no. 19, 1995, pages 4714-4727, XP002051922 * the whole document *	1	
A	WO 93 25234 A (UNIV CALIFORNIA) 23 December 1993 * the whole document *	1-5	
A	WO 98 19162 A (FRELINGER JEFFREY A ;NOVALON PHARMACEUTICAL CORP (US); KAY BRIAN K) 7 May 1998 * the whole document *	10	TECHNICAL FIELDS SEARCHED (Int.Cl.6)
T	FR 2 758 821 A (CENTRE NAT RECH SCIENT) 31 July 1998 * page 9, line 23 - page 10, line 17; claims 14,17,28 *	1-3,7	

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